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9 US-09-895-793-110
9 US-09-895-8144-110
10 US-09-745-288-110
110 US-09-759-143-110
110 US-09-759-143-110
110 US-09-030-666-110
110 US-09-030-666-110
110 US-09-030-666-110
110 US-09-103-110
9 US-00-913-704
110 US-09-759-143-704
110 US-09-759-143-704
110 US-09-938-422-1691
110 US-09-938-423-1691
110 US-09-938-423-1691
110 US-09-966-352-403
110 US-09-960-352-403
110 US-09-960-352-403
110 US-09-960-352-12483
                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09099823 Patent No. US20020018990A1 GENERAL INFORMATION:
                             RESULT 1
US-09-099-823-1
   February 9, 2003, 21:14:50; Search time 18.1938 Seconds (without alignments) 6148.496 Million cell updates/sec
                                                                                                                                                   US-09-099-823-1
236
1 GACGCCCAGIGACCTGCCGA......GCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*

1: /cqu2_6/ptodata//pubpna/USO7_PUBCOMB.seq;*
2: /cqu2_6/ptodata//pubpna/PCT_NBK_PUB.seq;*
3: /cqu2_6/ptodata//pubpna/PCT_NBK_PUB.seq;*
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13: /cqu2_6/ptodata//pubpna/USO8_PUBCOMB.seq;*
13: /cqu2_6/ptodata//pubpna/USO8_PUBCOMB.seq;*
14: /cqn2_6/ptodata//pubpna/USO8_PUBCOMB.seq;*
14: /cqn2_6/ptodata//pubpna/USO8_PUBCOMB.seq;*
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         408267 segs, 237001491 residues
                                                                                                                                                                                                                                                                                                                                                        Post-processing; Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                           Searched:
                                                                                              Run on:
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Sequence 1, Appli Sequence 4, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 26145, A Sequence 26145, A Sequence 9773, A Sequence 1178, Appli Sequence 11, Appli Sequence 110, Appli Sequence 110, Appli Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description US-09-099-823-1 US-09-9823-3 US-09-823-381-1747 US-09-951-845-1 US-09-951-845-1 US-09-91-845-1 US-09-91-868 US-09-91-868-1 US-09-91-868-1 US-09-91-978-1 US-09-91-978-1 US-09-968-1 US-09-963-790-1 US-09-32-88-1 SUMMARIES А DB Length Query Match

Score

Result No.

236 2236 2236 2236 236 237 24 25.28 25.28 25.28 25.28 25.28 26.28 26.28 26.28 26.28 27.28

APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COLEN, MARIELE
APPLICANT: COLEN, MARIELE
APPLICANT: COLEN, MARIELE
APPLICANT: FRIEDRAN, PAULA N.
APPLICANT: FRIEDRAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: RASS, MICHAEL N.
APPLICANT: RASS, MICHAEL N.
APPLICANT: RASS, MICHAEL N.
APPLICANT: RASS, MICHAEL N.
APPLICANT: SCHEFFEL, OND C.
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: SCHEFFEL, SCHEFFEL, CHRISTI
APPLICANT: SCHEFFEL, SCHEFFEL, CHRISTI
APPLICANT: SCHEFFEL, OPERATING SYSTEM: DOS SOFWHARE: RestSEN for Windows Version 2.0 CURRENY APPLICATION DATA: APPLICATION NUMBER: US/09/099,823 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-JUN-1997
ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl L. ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park STATE: IL COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wind COUNTRY: USA ZIP: 60064-3500 FILING DATE:

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61 TGGGTGTCACGCTCGGCCTGGCCGCTGCTCTTCACCTGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
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APPLICANT: COLETTS, TRACET L.
APPLICANT: COLETTS, TRACET L.
APPLICANT: ETIEDNAM, PAUJA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, STEVEN C.
APPLICANT: GRANADOS, STEVEN C.
APPLICANT: HOGES, STEVEN C.
APPLICANT: KRATOCHVIL, JOHN C.
APPLICANT: KRATOCHVIL, JOHN C.
APPLICANT: STEVENER, CHRIST, APPLICANT: STEVENER, STEPHEN D.
APPLICANT: STEVENER, STEPHEN D.
APPLICANT: STEVENER, STEPHEN D.
APPLICANT: STEVENER, STEPHEN D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 236; DB 10; Length 63
Best Local Similarity 100.0%; Pred. No. 1.1e-52;
Matches 236; Conservative 0; Mismatches 0; Indels
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     APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UNI-1997
ATORNEY AGENT INFORMATION:
NAME: BGACKAT, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park Road
STREET: IL
COUNTRY: USA
ZIP: G064-350
COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; Sequence 5, Application US/09099823
; Patent No. US20020018990A1
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                 TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
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US-09-099-823-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CAGGGACCTGGTACGTGAAGGCCATGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACGCCCAGTGACCTGCCGAGGTCGGCACAGAGACCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACGCCCAGTGACCTGCCGAGGTCGCCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 236; DB 10; Length 236; Best Local Similarity 100.0%; Pred. No. 9.2e-53; Matches 236; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COLETTS, TRACEL
APPLICANT: COLETTS, TRACEL
APPLICANT: COLETTS, TRACET I.
APPLICANT: CORDINA, PAULA N.
APPLICANT: GORDON, UULLAN
APPLICANT: GRANADOS, EDWRAD N.
APPLICANT: GRANADOS, STRVEN C.
APPLICANT: HOUGES, STRVEN C.
APPLICANT: RUSSELL, OHD D.
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: STROUTE, STEPHEN D.
APPLICANT: TU, HONG
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: PADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE PARK ROAD
CITY: Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM: DOS
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE:
FILLING DATE:
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: GOHEN, MARICICE
APPLICANT: COLPITS, TRACE I.
APPLICANT: FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.09-099-823-4
Sequence 4, Application US/09099823
Patent No. US20020018990A1
                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-09-099-823-1
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us-09-099-823-1.rni

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61 GARGARGARGAYATHACNGGNACNTGGTAYGTNAARGCNATGGTNGTNGAYAARGAYTTY 120
                                                                                                                                                105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                                                           CCGGAGGACAGGACCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 79 TGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 IGGAAGGTGGTCTGTCCTTCACCCTGGAGGAGGATATCACAGGGACCTGGTACGTGA 121
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Best Local Similarity 94.2%; Pred. No. 4.4e-12;
Matches 81; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09130663A

Sequence 16, Application US/09130663A

Patent No. 602016A

TITLE OF INVENTION:
APPLICANT: COALLIN, Darrell C.
FILE REFERENCE: 97-24

CURRENT PAPLICANION NUMBER: US/09/130,663A

CURRENT FILING DATE: 1998-08-05

EARLIER APPLICATION NUMBER: 60/054,867

EARLIER PILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 30

SOFTHAMES: FASTERE OF Windows Version 3.0

LENGTH: 147
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TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REPERENCE: 97-24
CURRENT APPLICATION INDERS: US/09/432,335
CURRENT FILING DAFE: 1999-11-02
EARLIER APPLICATION WUMBER: 09/130,663
EARLIER FILING DATE: 1998-086-06
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRALENG DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRALENG DATE: 1497-08-06
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 16
LENGTH: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: NEE-tagged linker US-09-130-663-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 AGGCCATGGTGGTCGATAAGGACTTT 147
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COTHER INFORMATION: NEE-tagged linker
US-09-432-335-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 AGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09432335 Patent No. 6143720 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                  225 AAGTTGGAAGC 235
                                                                                                                                                                                                                                            181 AARYINGARGC 191
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US-09-432-335-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 GAGGAGGATATCACAGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 ATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCTGCCCTGTCCTTCACCCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAARACNYTHTTYTHGGNGTNACNYTHGGNYTHGCNGCNGCNYTHWSNTTYACNYTH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Degenerate sequence derived from human zlipol OTHER INFORMATION: nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Degenerate sequence derived from human zlipol ornes in PRORMATION: nucleotide sequence in FORMATION: nucleotide sequence in Incartation in Location: (1)...(510) OTHER INFORMATION: n is any nucleotide US-09-614-022-5
                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.9%; Score 136.6; DB 3; Length 510; Best Local Similarity 60.7%; Pred. No. 2.8e-27; Matches 116; Conservative 35; Mismatches 40; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.9%; Score 136.6; DB 4; Length 510; Best Local Similarity 60.7%; Pred. No. 2.8e-27; Matches 116; Conservative 35; Mismatches 40; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09614022
Sequence 5, Application US/09614022
GENERAL INFORMATION
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFREENCE: 97-24
CURRENT PELLIGN DATE: 1200-07-11
CURRENT FILIGE DATE: 2000-07-11
FRIOR APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 60/054,867
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOSE: 30
SOFTWARE FASISEQ for Windows Version 3:0
LENGTH: 510
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILTING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
ID NO 5
LENGTH: 510
                                                                                                                                                                                                                                                         FEATURE:
NAME/KET: variation
LOCATION: (1)...(510)
O'THER INFORMATION: n is any nucleotide US-09-432-335-5
                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 AAGTIGGAAGC 235
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181 AARYINGARGC 191
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US-09-614-022-5
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Gaps

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Perfect score: Scoring table:

Run on:

Sequence:

Searched:

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Human BS124 specif.
Human reproductive
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Probe #25 used in
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                                                                                                                                              Human Zlipol DNA.
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BS124 specific EST clone 1730294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX07453 standard; cDNA; 236 BP.
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Human BS124 specif
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Human PR01283 (UNQ
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Human breast speci
                                                                                                                                                (without alignments) 6129.540 Million cell updates/sec
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                                                                                                                              February 9, 2003, 19:57:40; Search time 86.7066 Seconds
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1 GACGCCCAGTGACCTGCCGA.......GCGGTGGGAAGTTGGAAGCC 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseg/genesegn-embl/NA2002.DAT:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             OM nucleic - nucleic search, using sw model
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AAZ91770
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Database :

New isolated BS124 polynucleotides and polypeptides - used for

WPI; 1999-105623/09.

angiogenesis PRO1283 cDNA

Human B

Query Match 1

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and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelled a used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
                                                                                                                                                                                                                                                                                                                         61 PGGGTGTCACGCTCGGCCCTGGCCGTGCCTTCACCCTGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                             121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACGCCCAGTGACCTGCCGAGGTCGCCACACACACACTCTCGAGATGAAGACCCTGTTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BS124; breast; cancer; detection; diagnosis; prevention; treatment;
                                                                                                                                                                                                                                         1 GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCC
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                   Query Match 100.0%; Score 236; DB 21; Length 690; Best Local Similarity 100.0%; Pred. No. 2.8e-51; Matches 236; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                           Sequence 690 BP; 161 A; 208 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human BS124 specific EST clone 1730294IH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Pages 94-95; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX07456 standard; cDNA; 692 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0879354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TGGGTGTCACGCTCGGCCTGGCCCTGCCTCTCACCCTGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                            61 TGGGTGTCACGCTCGGCCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                 treating diseases or conditions
                                                                                                                                                                                                                                                                                                                                        1 GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; breast specific gene; breast specific marker; BSG; diagnosis; breast cancer; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236
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                                                                                                       The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                              Sequence 236 BP; 47 A; 63 C; 86 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human breast specific gene LS clone 1213903.
detecting, diagnosing, preventing or
of the breast, such as breast cancer
                                                             Claim 11; Page 94; 125pp; English.
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ID AAZ9.
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Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene therapy.
                                                                                                                                        Fong S;
Hillan KJ;
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                                                                                                        121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC
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100.0%; Score 236; DB 22; Length 738;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 236; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 738 BP; 209 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted; transmembrane; gene therapy; ss.
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99US-0144758.
99US-0145698.
                                                                                                                                                                                                                                                                                                                                                                                     AAF54313 standard; DNA; 738
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16-DEC-1999; 99W0-0530095.
05-JAN-2000; 2000W0-US00219.
06-JAN-2000; 2000W0-US00376.
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99WO-US28551
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Paoni NF, Roy MA,
e CK, Williams PM,
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20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
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Watanabe CK,
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                                                                                                                                                                                                                                                                                                                         61 TGGGTGTCACGCTCGGCCTGGCCGCTGTCCTTCACCCTGGAGGAGGAGGATATCA 120
                                                                                                                                                                                                                         121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                       Gaps
                                                                                         1 GACGCCCAGTGACCTGCCGAGGTCGGCACACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                         61 IGGGIGTCACGCTCGGCCTGCCCGCTGCCTTCACCCTGGAGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated BS124 polynucleotides and polypeptides - used for detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              181 CCAGGAAGGIGICCCCAGIGAAGGIGACAGCCCIGGGCGGIGGGAAGIIGGAAGCC 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of a consensus BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 236; DB 20; Length 692; larity 100.0%; Pred. No. 2.8e-51; Conservative 0; Mismatches 0; Indels 0
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           del Pa, Cohen M, Colpitts TL, Friedman PN;
Granados EN, Hodges SC, Klass MR, Kratoch
, Scheffel CP, Stroupe SD, Tu H;
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                    Pred. No. 2.8e-51;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BS124 specific EST clone consensus sequence.
100.08; Pic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX07457 standard; cDNA; 692 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                 Local Similarity 100. es 236; Conservative
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consensus; EST; ss.
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Russell JC,
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Matches 236;
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                                        Matches
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84 GCTGCCCTGTCCTTCACCCTGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 143
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         Best Local Similarity 96.3%; Pred. No. 1.3e-11;
Matches 78; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.3%; Score 76.2; DB 3; 96.3%; Pred. No. 1.3e-11; tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                               Sequence 24, Application US/09432335
Patent No. 6143720
GENERAL INFORMATION:
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION INDERS: US/09/432,335
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT APPLICATION NUMBER: 09/130,653
RAMLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1997-08-06
EARLIER FILING DATE: 1997-08-06
SARLIER OF EARLIER OF EARLIER OF SEQ ID NOS: 30
SOFTWARE: FASISED for Windows Version 3.0
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GENERAL INFORMATION:

TITLE OF INVENTION: LIPOCALIN HOMOLOG

FILE REPERENCE: 97-24

CURRENT PAPLICATION NUMBER: US/09/614,022

CURRENT FILING DATE: 2000-07-11

FRIOR PAPLICATION NUMBER: 09/130,663

PRIOR PAPLICATION NUMBER: 09/130,663

PRIOR APPLICATION NUMBER: 09/08-06

NUMBER OF SEX ID NOSE: 1999-08-06

NUMBER OF SEX ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 147
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                                                                                                                                                144 ATGGTGGTCGATAAGGACTTT 164
                                                                                                                                                                       127 ATGGTGGTCGATAAGGACTTT 147
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 78; Conservative
                                                                                                                                                                                                                                                   RESULT 11
US-09-432-335-24
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o
         Length 147;
    Score 78; DB 3; Length 147
Pred. No. 4.4e-12;
0; Mismatches 5; Indels
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Patent No. 6020163
GENERAL INFORMATION:
APPLICANT: CORKLIN, Darrell C.
TITLE OF INVENTION: ILPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION WUMBER: US/09/130,663A
CURRENT FILING DATE: 1998-08-06
BARLIER APPLICATION WUMBER: 60/054,867
BARLIER APPLICATION NUMBER: 60/054,867
SARLIER APPLICATION NUMBER: 60/054,867
SARLIER RESERVE OF SEX ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 147
                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09614022
Patent No. 6365116
GRNEAL INFORMATION:
APPLICANT: CONKIN, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILLE REFERENCE: 97-24
CURRENT PLING DATE: 1000-07-11
PRIOR APPLICATION NUMBER: 09/130, 653
PRIOR FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/054,867
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: N-terminal Flag linker
US-09-130-663-24
                                                                                                                                                          FEATURE: OTHER INFORMATION: NEE-tagged linker US-09-614-022-16
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      33.1%;
94.2%;
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ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 94.28
Matches 81; Conservative
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                                                                                                                                                                                                                                                             RESULT 9
US-09-614-022-16
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107 GGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGTAAG 158
               52 GGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTGGTGAAG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonuclectide primer: ZC13764 US-09-614-022-15
                                                                                                                                 Search completed: February 9, 2003, 22:05:01 Job time: 20.1542 secs
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Query Match 32.3%; Score 76.2; DB 4; Length 147; Best Local Similarity 96.3%; Pred. No. 1.3e-11; Matches 78; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.0%; Score 52; DB 3; Length 52; Best Local Similarity 100.0%; Pred. No. 2.2e-05; Matches 52; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonucleotide primer: ZC13764 US-09-130-663-15
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                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-09-130-663-15/C
Sequence 15, Application US/09130663A
Sequence 15, Application US/09130663A
SEMERAL INFORMATION:
APPLICANT CORALIN.
TITLE OF INVENTION: IPPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT FILING NUMBER: US/09/130,663A
CURRENT FILING DATE: 1998-08-05
REALIER APPLICATION NUMBER: 60/054,867
RANLIER FILING DATE: 1990-06
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 15
EMBITIES FILING DATE: 1990-06
SEQ ID NO 15
EMBITIES FILING DATE: 1991-08-06
SEQ ID NO 19
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GENERAL INFORMATION:
TITLE OF INVENTION: LIPPOCALIN HOMOLOG
TITLE REFERENCE: 97-24
CORRENT PAPLICATION NUMBER: US/09/432,335
CORRENT PAPLICATION NUMBER: 09/130,663
EARLIER PAPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 06/054,867
EARLIER PILING DATE: 1997-08-06
NUMBER OF SEQ ID NOTS: 1997-08-06
SOFTWARE: FALKED FOR NOS: 30
SOFTWARE: PASLEED for Windows Version 3.0
LENGTH: 52
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209-432-335-15/c

; Sequence 15, Application US/09432335

; Patent No. 6143720
                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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(without alignments)
4219.129 Million cell updates/sec
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236
1 GACGCCCAGTGACCTGCCGA......GCGGTGGGAAGTTGGAAGCC 236
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/cgn2_6/ptodata/1/ina/5a_comB.seq:*
/cgn2_6/ptodata/1/ina/6a_comB.seq:*
/cgn2_6/ptodata/1/ina/6a_comB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_comB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_comB.seq:*
        GenCore version 5.1.3
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                                                                                                                                                                                                                                                                                                                441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_NA:*
1: /cqn2 6/pt-04ata/1
                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                  Run on:
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0000000000

Sequence 110, App Sequence 110, App Sequence 110, App Sequence 110, App Sequence 110, App Sequence 110, App Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli		Length 522; Indels 0; Gaps 0; CGCTGCCTGTCCTTC 98 [
9410 4 US-09-605-785-110 9410 4 US-09-429-313-110 9410 4 US-09-552 E16a-110 9410 4 US-09-552-149A-110 9410 4 US-09-605-877A-100 9410 4 US-09-605-877-100 9410 4 US-09-605-785-704 571 6 516051-2 949 1 US-08-275-225-11 949 1 US-08-275-225-11 943 1 US-08-275-225-11 943 1 US-08-919-916-2 96 3 US-09-199-842-2 96 3 US-09-199-842-2 978 3 US-09-200-090-3 233 4 US-09-200-090-3 234 4 US-09-200-090-3 235 3 US-08-88-876A-1 575 4 US-09-472-880-1	ALIGNMENTS JS/09130663A rell C. OZALIN HOMOLOG BER: US/09/130,663A 89-08-05 87-08-06 indows Version 3.0	tch 13.2*, Score 196.4; DB 3; Length 522, 197; Conservative 0; Mismatches 1; Indels 0; G CTGGAGATGAAGACCTGTTCCTGGGTGTCAGGCTGGCCTGCCT
29 33 14.0 34 32 34 34.0 34 32 34 34.0 34 32 34 32.6 13.8 26 34 32.6 13.7 34 32.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.2 13.6 12.3 13.6 12.2 13.6 12.3 12.3 13.6 12.3 13.5 13.5 13.5 13.5 13.5 13.5 13.5 13	RESULT 1 US-09-130-663-1 US-09-130-663-1 Sequence 1. Application US/09130663A Fatent No. 6020163 GENERAL INFORMATION TITLE REPRENCE: 97-24 CURRENT APPLICATION NUMBER: 05/09/130,60 CURRENT APPLICATION NUMBER: 05/09/130,60 CURRENT FILING DATE: 1998-08-05 EARLIER FILING DATE: 1997-08-06 SOFTWARE: FELING DATE: 1997-08-06 NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 3 SEQ ID NO 1 LENGTH: 522 TENGTH: DAA SORGARISH: HOMO SAPIENS SORGARISH: HOMO SAPIENS SEAUTHE: 100-05/05/190/05/190/05/190/05/190/05/05/190/05/05/05/05/05/05/05/05/05/05/05/05/05	Query Matches Matches Matches 7 39 7 99 7 159 7 159 7 159 7 159 7 159 8 181 7 219 8 GENERAL APPLICAL

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159 GACTITCCGGAGGACCAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACGACCTGGGC 218
             99 ACCCTGGAGGAGGAGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAG 158
                                                                                                                  45 ATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGCCCTGCCCTGCCTTCACCCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 CCGGAGGACGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AIGAARACNYTNTTYINGGNGTNACNYTNGGNYTNGCNGCNGCNGCNGTNWSNTTYACNYTN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Degenerate sequence derived from human zlipol OTHER INFORMATION: nucleotide sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.9%; Score 136.6; DB 3 Best Local Similarity 60.7%; Pred. No. 2.8e-27; Matches 116; Conservative 35; Mismatches 40
                                                                                                                                                                                                                                                      RESULT 4

US-09-130-663-5

is Sequence 5. Application US/09130663A

patent No. 6020163

GENERAL INFORMATION:

ITTLE OF INVENTION: LIPCCALIN HOMOLOG

TITLE OF INVENTION: LIPCCALIN HOMOLOG

TITLE OF INVENTION: LIPCCALIN HOMOLOG

CURRENT PILLING DATE: 1996-08-05

SARLIER PEPLICATION NUMBER: 60/054,867

BARLIER PILLING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 30

SOFTWARE PRESEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09432335
Patent No. 643720
Patent No. 643720
Patent INPORMATION:
PITLE OF INFUNION: LIPOCALIN HOWOLOG
PITLE REPERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT PILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER PILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: variation

) LOCATION: (1)...(510)

OTHER INFORMATION: n is any nucleotide

US-09-130-663-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                 181 GGTGGGAAGTTGGAAGCC 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 GACTITCCGGAGGACAGGAGGCCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 CTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 CIGGAGAIGAAGACCCIGIICCIGGGIGICACGCICGGCCIGGCCGCIGCCCIGTC 98
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                                                                                                                                                                                                                                                                                                                                                                                          Length 522;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.2%; Score 196.4; DB 3; Best Local Similarity 99.5%; Pred. No. 6.7e-43; Matches 197; Conservative 0; Mismatches 1;
TITLE OF INVENTION: LIPOCALIN HOMOLOG
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER PILING DATE: 1997-08-06
SOFWWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09614022
Patent No. 6365716
GRENEAL INFORMATION:
APPLICANT: CORLII, DEATELL C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENY PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 522
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Best Local Similarity 99.55
Matches 197; Conservative
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (7)...(516)
US-09-432-335-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KET: CDS
; LOCATION: (7)...(516)
US-09-614-022-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ## Human; immune related disease; diagnosis; antinflammatory; cardiant; dermatorlogical; antiathritic; antichematic; immunosupressive; haemostatic; antithrematic; immunosupressive; haemostatic; antithrematic; immunosupressive; haemostatic; antithrematic; nootropic; neuroprotective; antianamenic; hepatotropic; virucide; antipardiat; antiallargic; antiallargic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic solaeosis; aarooldosis; didopathic inflammatory myopathy; systemic solaeosis; arrooldosis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; artoimmune thrombocytopenia; immune-mediated renal disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; fluten-sensitive enteropathy; autoimmune disease; fluten-sensitive enteropathy; autoimmune disease; fluten-sensitive enteropathy; mununulo disease; transplantation associated disease; immunological disease; transplantation associated disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease; ss.
                                                                                            61 TGGGTGTCACGCTCGGCCTGCCCGCTGCCTTCACCTTGGAGGAGGAGGATATCA 120
                                                                                                                                                          61 reserrence resecres ceres ceres ceres ceres ceres as series and ceres ceres ceres as a reserve ceres cere
                                                                                                                                                                                                                         121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                  1 GACGCCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGGAGATGAAGACCTCTTCC 60
                                                                                                                                                                                                                                                                                                                                                      181 CCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                                                                                                                                                                                           Human PRO1283 protein UNQ653 encoding cDNA SEQ ID NO:169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC58615 standard; cDNA; 739 BP.
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990S-0132371.
990S-0134287.
99WO-0S12252.
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99WO-US21547.
99WO-US23089.
99US-0162506.
99WO-US28214.
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-5066
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28-JUL-1999;
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15-SEP-1999;
15-SEP-1999;
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29-0CT-1999;
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30-NOV-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14~SEP-2000.
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A CANANA MARANA MARANA

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Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                       Henzel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TGGGTGTCACGCTCGGCCTGGCCGCTGCCTGTCCTTCACCCTGGAGGAGGAGAATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TGGGTGTCACGCTCGGCCTGGCCGTGTCCTTCACCCTGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Bebert C, He
Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Stewart TA, Tumas D, Wattanbe CK, Wood WI, Tan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 236; DB 21; Length 739; 100.0%; Pred. No. 2.8e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0%; Pred. No. 2.86
Matches 236; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Fig 73; 309pp; English.
                                                                                                                                                          06-JAN-2000; 2000MO-US00277.

06-JAN-2000; 2000MO-US00376.

11-FEB-2000; 2000MO-US03565.

18-FEB-2000; 2000MO-US04341.

18-FEB-2000; 2000MO-US04342.

22-FEB-2000; 2000MO-US04342.
                                                         99WO-US28565.
99WO-US30095.
99WO-US30999.
                                         99WO-US28564
                                                                                                                                            2000WO-US00219
                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-572271/53.
P-PSDB; AAB33450.
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
05-7AN-2000;
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121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180

181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236

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98105-0105593
9805-0105593
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9805-0105891
9805-0105807
9805-010502
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9805-0102965.
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980S-0103328.
980S-0103395.
980S-0103396.
980S-0103401.
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980S-0103711.
980S-0104257.
980S-0104987.
980S-0105000.
980S-0105004.
980S-0105104.
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98US-0103678
24.58P-1998
29.58P-1998
29.58P-1998
29.58P-1998
30.58P-1998
  Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
                                                                                                                                                              Human PRO1283 (UNQ653) cDNA sequence SEQ ID NO:161.
                                                  AAA37071 standard; cDNA; 739 BP.
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980S-0098749.
980S-0098730.
980S-0098803.
980S-0098813.
980S-0099814.
980S-0099598.
980S-0099598.
980S-0099562.
980S-0099754.
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9805-0099812
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9805-0100385
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98US-0100684.
98US-0100710.
98US-0100711.
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9805-0101014.
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9805-0101279.
9805-0101471.
9805-0101477.
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9805-0101477.
9805-0101479.
9805-0101741.
9805-0101741.
9805-0101741.
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                                                                                                                          08-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                             WO200012708-A2.
                                                                                                                                                                                                                                                                           Homo sapiens.
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01-53P-1998

01-53P-1998

02-53P-1998

02-53P-1998

03-53P-1998

09-53P-1998

09-53P-1998

09-53P-1998

09-53P-1998

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10-53P-1998

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10-53P-1998

11-53P-1998

11-53
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                                                                                         AAA37071;
                RESULT 7

AAA3 70711

AAA3 70712

AAA3 70713

AAA3 70714

AAA3 707
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angion, and angina, mycoardial infarctions, thromophlealitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 205; 567pp; English.
                                                                                                                                                                                                                                                                                                                                              2000WO-US34956.
2001US-0767609.
2001US-0796498.
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2001US-0854280.
2001US-0856280.
2001US-0866028.
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2001US-0870574,
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2001WO-US00000
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENENTECH INC.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-171999/22.
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FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GERBER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABB95525
  17-AUG 2000; 217-AUG 2000; 217-AUG 2000; 24-AUG 2000; 26 AUG 2000; 26 AUG 2000; 27-SEP 2000; 28 AUG 2000; 29 AUG 2000; 20 
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(GODD/)
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(WOOD/)
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(HILL/)
(MARS/)
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                                                                                                                                                                                                                                                                                                     AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, anglogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antianteriosclerotic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IGGGIGICACGCTCGGCCTGGCCGCTGCCCTGTCACCCTGGAGGAGGAGGATAICA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CAGGGACCTGGTACGTGAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGGGTGTCACGCTCGCCCTGGCCGCTGCCCTCCTCTCACCCTGGAGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACGCCCAGTGACCTGCCGAGGTCGGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                               Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 236; DB 21; Length 739; Best Local Similarity 100.0%; Pred. No. 2.8e-51; Matches 236; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiogenesis related cDNA PRO1283 SEQ ID NO: 205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                              Claim 2; Fig 99; 773pp; English.
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; 2000US-220624P.
; 2000US-220664P.
; 2000WO-US20710.
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(GETH ) GENENTECH INC.
                                                                                           WPI; 2000-237871/20.
                                                                                                                    P-PSDB; AAY99389.
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25-JUL-2000; 2
25-JUL-2000; 2
28-JUL-2000; 2
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ABB86072 to ABL88288 encode the PRO proteins given in ABB84817 to
MABB86003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulneary and antiatreinsolaterotic
activities, and can be used in gene therapy. The PRO polynucleotides,
cardiavascular, endothelial or angiogenic distorder in a mammal,
e.g. cardiac hypertrophy, trauma, cancer, age-related macular
c.g. cardiac hypertrophy, mycardial infarctions, thromopophietits,
imphangitis, tumour anglogenesis (such as breast carcinoma and liver
corcinoma) and wound healing. The PRO polynucleotides have applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapphing. ABL88259 to ABL88257 represent primers and
probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                           Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 205; 565pp; English.
  09-MAR-2001; 2001US-0802706.
14-MAR-2011; 2001US-0806689.
22-MAR-2001; 2001US-08167144.
05-APR-2001; 2001US-0828366.
10-MAY-2001; 2001US-0854208.
10-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001WS-087092.
30-MAY-2001; 2001WS-087092.
30-MAY-2001; 2001WS-087092.
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                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
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P-PSDB; ABB84919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial alisorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related meaular degeneration; arterial restenosis; angina; rhemmatoid arthritis; myocardial infarction; thrombophiebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                                                                                                                                                                                                                                      61 MGGGTGACCTGGCCTGCCCTGTCCTTCACCTGGAGGAGGAGGAGTATCA 120
                                                                                                                                                                                                                                                                                                                                                                   61 reserence or cescentes content of the content of
                                                                                                                                                                                                                                                                                                                                         121 CAGGGACCIGGIACGIGAAGGCCAIGGIGGICGAIAAGGACTIICCGGAGGACAGAGGGC 180
                                                                                                                                          1 GACGCCCAGTGACCTGCCGAGGTCGGCACACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                           0; Gaps
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Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO1283 cDNA sequence SEQ ID NO:205,
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20-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-22064P.
25-JUL-2000; 2000US-22064P.
23-AUG-2000; 2000US-054557.
24-AUG-2000; 2000US-054357.
24-AUG-2000; 2000US-054357.
24-AUG-2000; 2000US-054357.
24-AUG-2000; 2000US-054357.
24-AUG-2000; 2000US-054357.
24-CCT-2000; 2000US-056350.
24-CCT-2000; 2000US-056350.
24-CCT-2000; 2000US-056350.
24-CCT-2000; 2000US-056350.
24-CCT-2000; 2000US-0763537.
24-CCT-2000; 2000US-0763537.
25-DCC-2000; 2000US-0747259.
20-DCC-2000; 2000US-0747259.
22-DAN-2001; 2001US-0747559.
22-DAN-2001; 2001US-0747559.
22-DAN-2001; 2001US-0767669.
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                                                                      Similarity
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                                                                      Best Local Simi
Matches 236;
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                                               Query Match
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us-09-099-823-1.rng

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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPID-alpha. OBPS provide long-term retention (gradual release) of lipophilic compounds, so proflong the 'hold' of perfumes, deadorants etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect controlling volatilisation of an odorant, specifically in perfumes, controlling volatilisation of an odorant, specifically in perfumes, odorants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to sclubilisal lipophilic compounds, for treating hyperlipidemia or obesily, or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as a delayed release) but also for delivery acids, as food additives; as a delayed release) but also for delivery across the placental barrier foeto placental pathology (rupture of the amnictic membrane); and as antiallergic agents.
                                                   Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
                                                                                                                                                                 Location/Qualifiers
43..555
/*tag= a
/product= "odorant binding polypeptide OBPIIb-alpha"
            Nucleotide sequence of odorant binding polypeptide OBPIIb-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.2%; Score 234; DB 22; Length 676; Best Local Similarity 100.0%; Pred. No. 8.9e-51; Matches 234; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 113-114; 132pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gachon F;
                                                                                                                                                                                                                                                                                                                                     11-AUG-2000; 2000WO-FR02319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pitiot G, Lacazette E,
                                                                                                                                                                                                                                                                                                                                                                                                            (UYAU-) UNIV AUVERGNE. (PITI/) PITIOT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-202864/20.
P-PSDB; AAB67742.
                                                                                                                                                                                                                                                              WO200112806-A2
                                                                                                                               Homo sapiens.
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The present sequence encodes a human odorant binding polypeptide (OBP), C designated obPrID-beta (long form). OBPs provide long-term retention C designated obPrID-beta (long form). OBPs provide long-term retention CC (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, decodrants etc.. OBP polypeptides are used as binding proteins for hydropholic ligands (particularly odorants), as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; commetics or distilisation of an odorant, specifically in perfumes, octants or flavours, e.g. human pheromones, for binding to OBP also in CC analysis of complex perfume mixtures; to sclubilise lipophilic compounds; or trasporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery acids, as food additives; as a trasporter of pharmaceuticals, especially anticancer agents (providing coeto-placental pathology (rupture of the amniotic membrane); and as mitallergic agents.
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1.:540
A'ttag = A
/product= "odorant binding polypeptide OBPIIb-beta"
183 AGGAAGGTGTCCCCAGTGAAGGTGACACCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                        Nucleotide sequence of odorant binding polypeptide OBPIID-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 782 BP; 186 A; 226 C; 239 G; 131 T; 0 other;
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                                                                                                                     AAF80044 standard; cDNA; 782
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                                                                                                                                                                                         (first entry)
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P-PSDB; AAB67743.
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Query Match 99.2%; Score 234; DB 22; Length 782; Best Local Similarity 100.0%; Pred. No. 9.2e-51; Matches 234; Conservative 0; Mismatches 0; Indels 0

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3 CGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62

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transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or foeto-placental pathology (rupture of the amniotic membrane); and as
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                                                                                                                                                                                                                                                                                                                                                                      61 GGTGTCACGCTCGGCCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATGATCACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GGTGTCACGCTCGGCCTGGCCGCTGCCTTCACCTTGGAGGAGGAGGATATCACA 122
                                                                                                                                                                                                                                                                                                                                                                                                                             123 GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers

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/ Ariage a control binding polypeptide OBPIIa-beta"
                                                                                                                                                                                                                                                                                      3 CGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AGGAAGGTGTCCCCAGTGAAGGTGACACCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAACTTGGAAGCC 234
                                                                                                                                                                        Query Match 98.5%; Score 232.4; DB 22; Length 676; Best Local Similarity 99.6%; Pred. No. 2.3e-50; Matches 233; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of odorant binding polypeptide OBPIIa-beta
                                                                                                                                 Sequence 676 BP; 158 A; 199 C; 204 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 108-109; 132pp; French.
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                                                                                           antiallergic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-202864/20.
P-PSDB; AAB67739.
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AAF80040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
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                                                                               63 GGTGTCACGCTCGGCCTGGCCGTGCCTTCACCTTGGAGGAGGAGGAGGATATCACA 122
                                                                                                       182
                                                                                                                                                                                           9
    62
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/product= "odorant binding polypeptide OBPIIa-alpha"
                        1 GCCCAGTGACCTGCCGAGTCGCCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG
                                                                                                                                                              123 GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGAGACCC
CGCCCAGTGACCTGCCGAGGTCGGCAGCACAAGAGCTCTGGAGATGAAGACCCTGTTCCTG
                                                                                                                                                                                                                                                  Nucleotide sequence of odorant binding polypeptide OBPIIa-alpha.
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P-PSDB; AAB67738.
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Gachon F;

Pitiot G, Lacazette E,

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21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 GGGACCIGGIACGIGAAGGCCAIGGIGGICGAIAAGGACIIICCGGAGGACAGGACAGGACC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GGTGTCACGCTCGGCCTGCCTGCCTGTCCTTCACCCTGGAGGAGGAGATATCACA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62
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/product= "odorant binding polypeptide OBPIIa-gamma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAAGGIGICCCCAGIGAAGGIGACAGCCCIGGGCGGIGGGAAGITGGAAGCC 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of odorant binding polypeptide OBPIIa-gamma.
                                                                                                                                                                                                                                                                                                             Query Match 98.5%; Score 232.4; DB 22; Length 725; Best Local Similarity 99.6%; Pred. No. 2.3e-50; Matches 233; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                              Sequence 725 BP; 163 A; 222 C; 217 G; 123 T; 0 other;
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AAF80041
ID AAF80041 standard; cDNA; 741 BP.
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                                                                                                                                                                                                                                                   antiallergic agents.
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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPIRa-gamma. OBPs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (appoints or antagonists) of cellular lipopaloin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, commercial or disinfectant compositions; to screen compounds, especially controlling volatilisation of an obesity, or to supplement non-maternal milk when complex perfume mixtures; to screen compounds, especially anticance agents (providing transporter of pharmaceuticals, especially anticancer agents (providing transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier of controlling control the foctus; as a marker of pregnancy or controlling complex placents placed as a marker of pregnancy or controlling complex placents as a marker of pregnancy or controlling complex placents.) as a marker of pregnancy or controlling complex placents placents placed as expected as a control particle.
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                                                                                                               New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGTGTCACGCTCGCCTGGCCCGCTGCCCTTCACCCTGGAGGAGGAGGATATCACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CGCCCAGTGACCTGCCGAGGTCGGCACACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.5%; Score 232.4; DB 22; Length 741; 99.6%; Pred. No. 2.3e-50; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 741 BP; 165 A; 229 C; 220 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 3578.
                                                                                                                                                                                                                                                                       Claim 6; Page 109-110; 132pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC03580 standard; cDNA; 357 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.68
Matches 233; Conservative
WPI; 2001-202864/20.
P-PSDB; AAB67740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiallergic agents.
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AAC03580
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or PolyAk RNAs derived from 30 different tissues. ESP sequences usually correspond mainly to the 3' untranslated region (URF) of the mRNA because they are often obtained from oilgo-dr primed CDNA libraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from CDNAs with intact 5' ends and can therefore be used to obtain full length green was an ender an equal sequences may be sequenced and squanchic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining CDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IGGGTGTCACGCTCGGCCTGGCCGCTGTCCTTC-ACCTTGGAGGAGGATATC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ACAGGGACCIGGIACGIGAAGGCCAIGGIGGICGAIAAGGACTIICCGGAGGACACAGGAGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 ACAGGAACCTGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACGCCCAGTGACCTGCCGAGGTCGGCACAGAGCTCTGGAGATGAAGACCTGTTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.2%; Score 224.6; DB 21; Length 357; Best Local Similarity 99.2%; Pred. No. 2.1e-48; Matches 235; Conservative 1; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 357 BP; 82 A; 88 C; 123 G; 62 T; 2 other;
                                                                                                       Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 3578; 71pp + CD-ROM; English.
                      99US-0122487.
                                                                                                                                               WPI; 2000-500381/45.
P-PSDB; AAG03574.
                                                             (GEST ) GENSET.
                 26-FEB-1999;
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Search completed: February 9, 2003, 22:02:06 Job time : 94.7066 secs

180 CCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.		February 9, 2003, 22:02:40; Search time 768.819 Seconds (without alignments) 8933.518 Million cell updates/sec
versic - 2003	v model	3:02:40
Core 1993	ing sv	33, 22
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	OM nucleic - nucleic search, using sw model	Run on:

	(Without disjunctor) 8933.518 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-099-823-1 236 1 GACGCCCAGTGACCTGCCGAGCGGTGGGAAGTTGGAAGCC 236
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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45																		
Listing first	GenEmbl:* 1: gb_ba:*	2: gb_htg:*	3: gb_in:*	4: gb_om:*	5: gb_ov:*	6: gb_pat:*	7: gb_ph:*	8: gb_pl:*	9: gb_pr:*	10: gb_ro:*	11: gb_sts:*	12: gb_sy:*	13: gb_un:*	14: gb_vi:*	15: em_ba:*	16: em_fun:*	 18: em_in:*	19: em_mu:*
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	em_om:*	em_or:*	em_ov:*	em_pat:	em_ph:*	em_p1:*	em_ro:*	em_sts:	*:un_mə	em_vi:*	ł	htg		em htg	em_htg_1		em_htg_n	- 1	em_sy:*	em_htgo_hum	em_htgo_mus	em htgo	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	No.	Score	Match	Length	BB	TD.	Description	
	н	236	100.0	739	9	AX454620	AX454620 Sequence	
	C) (236	100.0	739	ωı	AX491098	AX491098 Sequence	
	m <	234	20.00	9/9	ه م	AX083544	AXO83544 Sequence	
	# LC	234	0.00	782	v re	AX083546	AX083546 Sequence	
	ou o	234	99.5	782	0	HSA251027	AJ251027 Homo sapi	
	7	232.4	98.5	9/9	9	AX083536	nce	
	∞ (232.4	98.5	676	on I	HSA251021	AJ251021 Homo sapi	
	y (-	232.4	28.0	725	00	AXU83538 HSA251022	A.1251022 Homo sapi	
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	T 7	130.0	y	13591	o v	AKZU4U81 ax083551	AXO83551 Segmence	
	17	120.4	51.0	13591	9	HSA251025	AJ251025 Homo sapi	
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	0 50	120.4	21.0	102473	0	AC002320	AC002320 Homo sapi	
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	23.5	118.0	200	10664	0 0	HSA251029	AJ251029 Homo sapi	
	25	118.8	50.3	38017	o	AC000396	AC000396 Genomic s	
-	c 25	118.8	50.3	153231	O	AL161452	AL161452 Human DNA	
	26	118.8	50,3	167831	(7)	AC016427	AC016427 Homo sapi	
	27	114	48 8 9	542	6	AX083548	AXU83548 Sequence	
	200	114	4 d 5 d 5 d	242	ש ת	#SAZ31020	AXO83542 Segmence	
•	67 0.6	114	4 4	603	σ	HSA251023	AJ251023 Homo sapi	
	31	78	33.1	147	9	AR204090	유	
	32	76.2	32.3	147	9	m	AR204098 Sequence	
	33	8.8	29.5	732	200	RATTY2G12A	M/6/34 Rat odorant	
	д. 4- п	27.75	2.47	7.38	30	BCUZ/556 BSymco	X62418 H saniens m	
	n ve	53.6	22.7	784	n o	HUMHTP	M90424 Human tear	
	37	53.6	22.7	189661	~	AC125365	Ø	
	38	52.4	22.2	168384	~	AC121473	AC121473 Rattus no	
	G 33	23	22.0	25	9	AR204089	AR204089 Sequence	
	40	27	22.0	770	6	AX214532	poe	
	41	22	22.0	770	თ -	A C	Xb/b4/ H.saplens m	
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						ALIGNMENTS		
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	AX454620		AX454620			739 bp DNA	linear PAT 06-JUL-2002	O
	DEFINITION	z		205 from		Patent W00208284.		
	ACCESSION VERSION		54620 54620.1	GI:2171	(4)	934		
	SOURCE	human	an.					
	ORGANISM		Homo sapiens Eukaryota; M	metazoa;		Craniata;	144	
	REFERENCE		maila;	Eutheria	•-	ruin	nge	
	AUTHOR		Baker, K.P. Godowski.F		ra,	Gerber, H., Gerri L., Hillan, K.J.,	., Godda	
		Paoi	Paoni, N.F.,	., Stephan, J.P.	an,	, Watanabe, C.K.,	Williams, P.M., Wood, W.I.	

us-09-099-823-1.rge

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ELPRROHYIFYCKDQHHGGLLHMGKLVGRNSDTNREALEEFKKLVQRKGISEEDIFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 28-FEB-2001
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Homo sapiens mRNA for putative odorant binding protein b-a (OBPIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 676)

Pritot, G., Lacazette, E. and Gachon, F.

Polypeptides and proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and
uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: WO 0112806-A 9 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
L. 676
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/note
                                 61 TGGGTGTCACGCTCGGCCTGGCCGCTGCCTTCACCCTGGAGGAGGAGGATATCA 120
                                                            121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GETGTCACGCTCGGCCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GGTGTCACGCTCGGCCTGGCCGCTGTCCTTCACCCTGGAGGAGGAGGAGGATATCACA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CGCCCAGTGACCTGCCGAGGTCGGCACACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62
                                                                                                                                                                       181 CCAGGAAGGTGTCCCCAGTGAAGGTGACACCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                                                                            183 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGGAAGTTGGAAGCC 236
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Best Local Similarity 100.0%; Pred. No. 3.6e-41;
Matches 234; Conservative 0; Mismatches 0; Indels
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TITLE
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Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis
Berneth: WO 0208284-8 205 31-7Mx-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Genber, Hanspeter (US); Gerritsen, Mary E. (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Paoni, Nicholas F. (US); Atsphan, Jean-Philippe F. (US); Maranabe, Colin K. (US); Milliams, P. Mickey (US); Wood, Williams I. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0200690-A 205 03-JAN-2002;
Genentech, Inc. (US)
Location/Qualifiers
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Sequence 205 from Patent W00200690.
AX491098 AX491098.1 GI:22323886
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 207 c 205 g 117
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a 207 c 205 g 117
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VKAWVDKDFPEDRRPRKVSFVKVTALGGGKLEATFTFWREDRCTGKKILMRKTEEPG
XYSACLSAVENDGTPALMEALAIDFILKLRIGTRRPRIRWGQEAHVPAGAAQBGPLH
LLLQRPRAPMPRAPHGRAGG"
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1 (bases 1 to 782)

Lacazettes. E., Gachon, A.M. and Pitiot, G.

A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
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Direct Submission
Sibnitted (26-oCT-1999) Laboratoire de Biochimie Medicale - INSERM
Sibnitted (26-oCT-1999) Laboratoire de Biochimie Medicale - INSERM
S184, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
                                             1 (bases 1 to 782)
Pitof.G., Lacazette,E. and Gachon,F.
Politof.G., Lacazette,E. and Gachon,F.
Polypeptides thuman proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and
uses thereof
Patent: WO 0112806-A 11 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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-do.: 540
/note="cDNA2098 (782) - forme longue (hOBPLIb-beta)"
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AJ251027.1 GI:6900078
GDRITh gene; odorant binding protein.
Homo sapiens.
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HSA251027
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RPRKVSPVKVTALGGGKLEAFFTMREDRCIQKKILMRKTEBPRKYAAVGRKLMTLO
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                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 676)
Lacazette, E., Gachon, A.M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934; differential expression in the oral and genital spheres
                                                                                                                                                                                                                                                                                                             Gachon.A.M.

Gachon.A.M.

Burect Submission

Submitted (26-027-1999) Laboratoire de Biochimie Medicale - INSERM
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE

Location/Qualifiers
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10607840
gene).
AJ251026.
AJ251026.1 GI:6900076
OBPIID gene; odorant binding protein.
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/Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9934"
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Sequence 11 from Patent W00112806.
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Location Pouralifiers

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(Ab_xref="taxon:9606"

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/protein_id="cap13181."
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1 (bases 1 to 676)

Lacazette, E., Gachon, A.M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and gental spheres

Fum. Mol. Genet. 9 (2), 289-301 (2000)
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                                                                             Score 232.4; DB 6; Length 676; Pred. No. 7.9e-41; 0; Mismatches 1; Indels 0;
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OBPIIa gene; odorant binding protein.
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Best Local Similarity 99.6%;
Matches 233; Conservative (
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Best Local Similarity 99.69
Matches 233; Conservative
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protein_id="0.41"
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RPRAVEDRYSACHERNERGERARFFFRREDRCIOKKILMRKTEEPGRYSACLEARFPEDR
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 676)

Pitiof.c., Lacasette.E. and Gachon,F.

docant-binding human proteins fixing hydrophobic ligands;

polypeptides and polynucleotides coding for said polypeptides and polynetises.

Docanie: WO 0112806-A 1 22-FEB-2001;

Universite d'Auvergue (FR); Pitiot, Gilles (FR)

1. 076
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1. .782
Organism="Homo sapiens"
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/chromosome="9"
/map="934"
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/db_xref="taxon:9606"
43. .555
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/db_xref="GI:13185347"
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/gene="OBPIIb"
43. .540
/gene="OBPIIb"
/codon_start=1
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222 c 217 g 123 t
                  HSA251022 725 bp mRNA linear PRI 02-FEB-2000 Homo sapiens mRNA for putative odorant binding protein ab (OBPIIa
                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 725)

Lacacette, E., Gachon, A.M. and Pitiot, G.

A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
                                                                                                                                                                                                                                              genital spheres

Mun. Mol. Genet. 9 (2), 289-301 (2000)

10607840

2 (bases 1 to 725)

Gachon A.M.

Direct Submission

Submitted (26-007-1999) Laboratoire de Biochimie Medicale - INSERM
0384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE

1. 725
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AJ51022.1 GI.6900068
OBPIIG gene; odorant binding protein.
Homo sapiens
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AX083540 AX083540.1 GI:13185350
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43. .482
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222 c 217 g 123 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
Priiot, G., Lacazette, E. and Gachon, F.
Odorant-binding human proteins fixing hydrophobic ligands:
Polypeptides and polymucleotides coding for said polypeptides and
uses thereof
                                                                           63 GGTGTCACGCTCGGCCTGCCCTGCCCTTCACCCTGGAGGAGGAGGATATCACA 122
                                                                                                61 GETGTCACGCTCGGCCTGGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 120
                                                                                                                                           123 GGGACCIGGIACGIGAAGGCCAIGGIGGICGAIAAGGACTIICCGGAGGACAGGGCCC 182
                                                                                                                                                                  1 GCCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTG 60
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Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 0112806-A 3 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 725
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                                                                                                                                                                                                                                                                                                                                 DNA
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AX083538.1 GI:13185348
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Matches 233;
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us-09-099-823-1.rge

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U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
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99.5%; Pred. No. 5.4e-33;
iive 0; Mismatches 1;
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Sequence 1 from patent US 6365716.
AR204078 GI:21500632
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conthin.D.C.

Antibodies to lipocalin homologs

Patent: US 6365716-A 1 02-APR-2002;

Location/Qualifiers
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132 c 172 g
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43. .729
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                          43 729
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REPGYDDYTYCKOGRAGGLAYMGKLIAFDA
PWAKLRNWGSTROSRRRIFGCPCRREAAFSNTRQPFGLALQSPPTHQTQSPDHLDLPS
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1 (bases 1 to 741)

Lacazette, E., Gachon, A.M. and Pitiot, G.
A novel human odozant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
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Gachbu, A. M.
Direct Submission
Submitted (26-0CT-1999) Laboratoire de Biochimie Medicale - INSERM
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Pred. No. 7.9e-41;
0; Mismatches 1; Indels 0
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Hum. Mol. Genet. 9 (2), 289-301 (2000)
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OBPIIn gene; odorant binding protein.
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Best Local Similarity 99.6%;
Matches 233; Conservative
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                 Homo sapiens
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S7.99; Score 136.6; DB 6; Length
Best Local Similarity 60.78; Pred. No. 5.3e-20;
Marches 116; Conservative 35; Mismatches 40; Indels
Unknown.

GSM Unknown.

BUCB I (Dases) to 510)

HORSE CONKIN.D.C.

ITLE Antibodies to lipocalin homologs
JOURNAL Patent: US 6365716-A 5 02-ARP-2002;

"TRES - Location, Qualifiers
1. 510

/organism="unknown"
/organism="unknown"
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Job time : 780.819 secs
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181 AARYINGARGC 191
                               SOURCE
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Location/Qualifiers

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Anote="unnamed protein product"

Abaxref="di-chol37778.1"

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                         99 ACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAG 158
                                                    61 ACCCTGGAGGAGGAGGATATCACAGGGACCTGGTAAGGCCATGGTGGTGGTGGTAAAG 120
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Use of human phermone polypeptides
Patent: WO 0223201-A 1 21-MAR-2002;
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Sequence 5 from patent US 6365716.
AR204081 GI:21500636
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122 AGGGACCTGGTA-CGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGG
77 GGGTGTCACGCTCGGCCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCAC 136
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                                                                                                                                                 181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGGAAGTTGGAAGCC 236
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                                                                                                                                                                                                                                                                                                                                  APPLICART: LOK, SI
APPLICART: POSTER, Donald C.
APPLICART: POSTER, Donald C.
TITLE OF INVENTION: Use of Human Phermone Polypeptides
FILE REPERENCE: 00-65
CURRENT APPLICATION NUMBER: US/09/951,845
CURRENT FILING DATE: 2001-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                        Sequence 1, Application US/09951845; Patent No. US20020098497A1; GENERAL INFORMATION:
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Patent No. US20020018990A1
GENERAL INFORMATION:
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RUSSELL, JOHN C.
SCHEFFEL, CHRISTI
STROUPE, STEPHEN D.
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KLASS, MICHAEL R.
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; LOCATION: (8)...(517)
US-09-951-845-1
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US-09-951-845-1
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US-09-099-823-2
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Sequence 1147, Application US/09833381
GENERAL INFORMATION
GENERAL INFORMATION: Neith E.
TITLE OF INVENTION: No. US20020132090alel Nucleic Acid and Protein Homologs
TILE REFERENCE: S800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 692;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 236; DB 10; Best Local Similarity 100.0%; Pred. No. 1.1e-52; Matches 236; Conservative 0; Mismatches 0;
                                      CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-701-1997
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
RESISTRANCE/OCKET NUMBER: 51-00.US.PI
TELECHOMBINICATION INCREME: 610.US.PI
TELECHONIS: 847/935-1729
TELEPRIS: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOGTWARE: FestSEQ for Windows Version 3.0
SEQ ID NO 1747
LENGTH: 336
  APPLICATION NUMBER: US/09/099,823
                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACKERISTICS:
EBRGTH: 692 base pairs
TYPE: nucleic acid
STRANBENESS: single
TOPOLOGY: linear
US-09-099-823-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-833-381-1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-833-381-1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: 1
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Gaps

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55 GCGTCCTGCGCCGGCCGTGTCGAACGACCCCTGAAGAAAGTGCCCGGGGTCGCGGCCGCCC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 GTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTGGGTGTC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 TGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 cresrescescescercasecescescraccaserressescesces 221
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/0-03-21
PRIOR APPLICATION NUMBER: 60/0-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
SOFTWARE RESERVE FOR WINDOWS VERSION 4.0
SEQ ID NO 786B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Pseudomonas aeruginosa EFATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.2%;
Best Local Similarity 50.9%;
Matches 85; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (1)...(2379)
US-09-815-242-7868
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: 99
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LENGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGGAAGTTGGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAGGAGGCCCAGGAAGGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 52.5%; Score 124; DB 10; Length 245; Best Local Similarity 100.0%; Pred. No. 16-23; Makethes 124; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baselbeck, Robert
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Mananoto, Robert T.
APPLICANT: Mananoto, Robert T.
APPLICANT: Promanco, Robert T.
APPLICANT: Promanco, Robert T.
APPLICANT: SIGNATION: Prockaryotes
FILLE REFERENCE: BLITAN, JOHA
CURRENT PRILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                               ZIF: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TIPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TEM Compatible
COMPUTER: TEM Compatible
COMPUTER: TEM COMPATIBLE
COMPARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823
FILING DATE:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UUN-1997
ATTORNEY FASTER INFORMATION:
ATTORNEY FASTER INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Becker, Cheryl L.
REGISENTON NUMBER: 35,441
REFERENCE/TON TOTALER: 6120.US.Pl
TELECOMMUNICATION TRYORMATION:
TELEPHONE: 847/938-1729
TELEPEN: 847/938-1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7868, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
US-09-099-823-2
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AGCC 236
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Score 35.8; DB 10; Length 2379; Pred. No. 1.1; 0; Mismatches 82; Indels 0;

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GENERAL 186-09-923-876-3670

Sequence 3670, Application US/09923876

Sequence 3670, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalgud, Raghurath V.

APPLICANT: Application POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-012-1 CON

CURRENT FILING DATE: 1099-04-21

PRIOR PILICATION NUMBER: 09/298,329

PRIOR PILICATION NUMBER: 09/298,329

PRIOR PILICATION NUMBER: 60/208,331

PRIOR PILICATION NUMBER: 60/208

PRIOR PILICATION NUMBER: 60/208

PRIOR PILICATION NUMBER: 60/208

SERON REPLICATION NUMBER: 60/208

SOFTHARE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700405401H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: a, t, c, g, or other US-09-923-876-3670
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DB 10; Length 320;

14.9%; Score 35.2;

us-09-099-823-1.rnpb

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Sequence 2645, Application US/09864761

Sequence 2645, Application US/09864761

Sequence 10. US202004976341

GENERAL INFORMATION:

APPLICAMT: Penn, David R.

APPLICAMT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USBFUL. FT TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: QUARER: US/09/864,761

CURRENT ELLING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US/00/180,312
                                                                                                                                                                                       84 GCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 143
                                                                                                                                                                                                                                                                  58 GATACCCCAGCCTTGGGAAAGGACACTGTGGCTGTGTCAGGGAAATGGTATCTGAAGGCC 117
                                                                                                                                                                                                                                                                                                                                                                144 ATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCCAGGAAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                118 ATGACAGCAGAGCAGGAGGTGCCTGA----GAAGCCTGACTCAGTGACTCCCATGATC 171
                                                                                                        6; Gaps
         Query Match 14.8%; Score 35; DB 10; Length 525; Best Local Similarity 56.9%; Pred. No. 1.4; Matches 87; Conservative. 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 49117
SOFTWARE. Annomax Sequence Listing Engine Vers. 1.1
SEQ ID NO 25145
LENGTH: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 GIGACAGCCCIGGGCGGIGGGAAGTIGGAAGCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 CICAAAGCCCAGAAGGGGGGCAACCIGGAAGCC 204
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNGER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR PRIING DATE: 2000-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-07
PRIOR PRILORION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-07
PRIOR PRILORION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PLICATION NUMBER: PCT/USO1/00667
PRIOR PRIOR PLICATION NUMBER: PCT/USO1/00667
PRIOR PRIOR PLICATION NUMBER: PCT/USO1/00667
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ORGANISM: Homo sapiens
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US-09-864-761-26145
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                                                                                                                                                                                                                                                                                                                                                                                              123 CCGTTGGCGACATGGAGCCGTTGGCCGTGATGCCGTGAACAAGTTCCTGCAGCCCAAGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 AGCICTICAAGGICGICGAGGCGCCCGCGCCCGGGGCCGICCAAGAAGAAGAAGG 242
                                                                                                                                                                                                                                                                                                         88 CCCTGTCCTTCACCCTGGAGGAGGAGATATCACAGGGACCTGGTACGTGAAGGCCATGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 IGGICGATAAGGACTITCCGGAGGACAGGAGGCCCAGGAAGGIGTCCCCAGIGAAGGIGA 207
                                                      0; Gaps
                                                                                                                                      28 AGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09374671
| Patent No. US20020012963A1
| GENERAL INFORMATION:
| APPLICANT: Manieczny, Jay P. |
| APPLICANT: Kanieczny, Andrzey | APPLICANT: Branct, Andrew W. |
| APPLICANT: Branct, Andrew W. | ALBERGANDENCE INVENTION: Dander and Uses Therefor | NUMBER OF SEQUENCES: 104 |
| NUMBER OF SEQUENCES: 104 |
| STREET: 28 State Street | STREET: 28 State Street | STREET: 28 STATE STREET: 200 STREET: 200 STREET | STREET: 200 STREET | STREET: 200 STREET | STREET: 200 STREET | STR
Best Local Similarity 47.8%; Pred. No. 1.1;
Matches 100; Conservative 0; Mismatches 109; Indels
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WATCHWEY, AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION UNDERE: 36,207
REFERENCE/DOCKET WINBER: 111-026CP (IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 272-7400
TELEFONE: (617) 274-214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRAFACTER(STICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDENDES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 CAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
GURRARY APPLICATION NUMBER: US/09/374,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 CTGGTCGCGGGGAGTGACGACGATTCC 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: mat_peptide
; LOCATION: 79.525
US-09-374-671-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1..525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 28 St
CITY: Boston
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TS-09-374-671-1
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us-09-099-823-1.rnpb

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Gaps
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COTER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BUNG, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BUNG, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HERAR, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HERAR, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HERAR, SIGNAL = 1.7

US-09-864-761-9773
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APPLICANT: HUrban, Patrick
TITLE OF INVERTION: Expressed Sequences of Arabidopsis
TITLE OF INVERTION: thaliana
FILE REPERENCE: 2024 (PARA-013FRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 9773
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Patent No. US20020059663A1
GENERAL INFORMATION:
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Hass, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
Davis, Keith R.
Allen, Keith
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Matthew, Abraham V.
Ledford, Brooke L.
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Rameaka, Joshua G.
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Hamilton, Carol M.
Price, Jennifer L.
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-770-149-978/c
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APPLICANT:
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: GENE EXPRESSION ANALYSIS BY MICROARRAY
ITLE OF INVESTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TILE OF INVESTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STREET APPLICANTON NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-29
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-01-04
PRIOR PILING DATE: 2000-08-26
PRIOR PILING DATE: 2000-08-26
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
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CTHER INFORMATION: MAP TO ALO08723.8

CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BULLY SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1

OTHER INFORMATION: SIGNAL = 2.1

US-09-864-761-26145
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 201-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 52.0 es 78; Conservative
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US-09-864-761-9773
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80 GGCCGCTGCCCTGCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-886-055-194/c
US-09-886-055-194/c
Sequence 194, Application US/09886055
Fatent No. US20020132273A1
GENERAL INFORMATION:
APPLICANT: STRYEN, LUBERT
APPLICANT: ZOZGUZA, SERGER
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
FITLE REFERENCE: 078003-0777150
FILE RECEPTOR NUMBER: US/09/886.055
CURRENT FILING DATE: 2001-06-22
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                                                                                                                 58; Indels
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Matches 64; Conservative 0; Mismatches 50; Indels
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 194
LENGTH: 948
                                                                                Best Local Similarity 54.3:
Matches 69; Conservative
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US-09-886-055-194
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US-09-738-626-1278
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APPLICANT:
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APPLICANT:
                                                Query Match
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14.5%; Score 34.2; DB 10; Length 600;
Best Local Similarity 54.3%; Pred. No. 23.5
Best Coal Sinilarity 0.1 Mismatches 69; Conservative 0; Mismatches 89; Indels 0;
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APPLICANT: Allen, Keith
APPLICANT: Allen, Keith
APPLICANT: Allen, Keith
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Ar
TITLE OF INVENTION: 2001-01-26
PRIOR PILLING DATE: 2001-01-26
PRIOR PILLING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 999
SOFTWARE FEASTED for Windows Version 4.0
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
WINBER OF SEQ ID NOS: 999
SOFTWARE: RESISED for Windows Version 4.0
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Patent No. US20020059663A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(600)
COHER INFORMATION: n = A,T,C or G
US-09-770-149-978
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; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-885
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana
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Rameaka, Joshua G.
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Price, Jennifer L.
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Kricker, Maja
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An, Yong-Qiang
Hamilton, Carol
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US-09-770-149-885
                                                                                                                                                                                 600
                                                                                                            SOFTWARE: FE
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SEQ ID NO 885
                                                                                                                                                                                                                     TYPE: DNA
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| PRIOR FILING DATE: 1999-12-16
| PRIOR APPLICATION NUMBER: JP 00/159162
| PRIOR APPLICATION NUMBER: JP 00/28098
| NUMBER OF SEQ ID NOS: 7059
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ALS 67423 ALE 67423
BG493366 602537121
BR237420 894045A07
BE121219 89406A07
BE121219 89406A07
BE121219 89406CD08
BG918346 1030070C0
B1991345 1024039C0
B1970625 20182 NA
B170625 RA3-18020
B175107 AV33930 AV33930 AV33930 AV433930 AV433930 AV433930 AV433930 AV433930 AV433930 AV43399 AV43399 AV43399 AV43399 AV43399 AV43399 AV43399 AV43399 AV433260 B123751 AV43399 AV43399 AV43399 AV43320 AV4
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I (bases I to 337)
Smith, T. D., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Mray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.E., Beaton, M.P., Laegreid, W.W., Rohrer, G.A., Chiko-McKown, C.G., Pertea, G., Holt, I., Stammychews, S., Ling, F., Ouackenbush, J. and McGele, J.W.
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Pan trogl
EST351590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA librarias and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE193883 337 bp mRNA linear 245514 MARC 2BOV Bos taurus cDNA 5', mRNA sequence. BE193883.1 GI:11077252
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                                                                                                                                                                                                       B1538748
BF706258
BE753611
B1046625
CNS02FAE
BF251756
AV639302
AV392771
BM488076
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AV433303
AV435909
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AV432260
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  RESULT 1
BF193883
LOCUS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
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MEDLINE
COMMENT
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  BF193883 245614 MA
R47029 Y358 Rat in
BB618259 BB618259
A1877465 uGldd09.r
AW513637 xo47h10.x
BB028765 BB028765
                                                                                  February 9, 2003, 22:05:30; Search time 656.018 Seconds (without alignments) 5826.269 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                US-09-099-823-1
236
1 GACGCCCAGTGACCTGCCGA.......GCGGTGGGAAGTTGGAAGCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                              32308132
            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                    16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                             OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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R47029
BB618259
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Gapop 10.0 , Gapext 1.0
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em_gss_pin:*
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Maximum DB seq length: 2000000000
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gb_est4:*
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603
519
532
626
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24.7
24.2
21.9
21.9
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Perfect score:
Sequence:
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68.8
58.4
57.2
51.8
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Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria: Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases I to 603)

R Arakwar, T. Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haramcho, K., Hori, F., Ishii, Y., Ito, M., Kwai, J., Kono, H., Kouda, M., Koya, S., Matayamar, T. Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, J., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, T., Tanaka, T., Toya, T., Muramatau, M. and Hayashizaki, Y., Rakeda, T., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
1..494
/organism="Rattus norvegicus"
/strain="Sprague-Dowley"
/strain="Sprague-Dowley"
/db_xref="Azon:10116"
/clone="Yexcor:10116"
/lab_host="Yexcor: Bluescript II SK -; Site_1: Bco RI; Site_2: /note="Veccor: Bluescript II SK -; Site_1: Bco RI; Site_2: /note = welcor plue sortion and the entire pulp of the maxillary adjocal portion and the entire pulp of the maxillary adjocal portion and the entire pulp of the maxillary adjocal portion and the entire pulp of the II vector (Stratagene) by use of poly A+ RNA from these tissues. The phage CDNA library was converted into a Bluescript phagemid cDNA library was converted into a Bluescript pagemid cDNA library by in vivo excision by the Exassist/SoLR system (Stratagene).
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BB618259 RIKEN full-length enriched, 6 days neonate head Mus
musculus cDNA clone 5430417003 5', mRNA sequence.
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UKE:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 GGATATCACAGGGACCTGGTACGTGAAGGCCCATGGTGGTCGATAAGGACTTTCCGGAGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 CAGGAGGCCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.2%; Score 68.8; DB 14; Best Local Similarity 60.9%; Pred. No. 1.7e-06; Matches 112; Conservative 0; Mismatches 72;
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BB618259.1 GI:16457878
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                     145 a
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               source
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JOURNAL
COMMENT
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BB618259
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         v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRimers
                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="texon:9913"
/clone_lib="MaxC_2Boy"
/tissue_lip="maxC_2Boy"
/tissue_lip="pooled"
/lab_host="Pull0"
/note="weetor: powr SPORT6; Site_l: Not!; Site_2: Sall;
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
/2 a 110 c 110 g 45 t
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Marsuki,Y., Nakashima,M., Amizuka,N., Warshawsky,H., Goltzman,D., Yamada,K.M. and Yamada,Y.
A compilation of partial sequences of randomly selected cDNa clones
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 CTGCCCT------GTCCTTCACCCTGGAGGAGGAGGATATCACAGGGA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.1%; Score 94.6; DB 12; Length 337; 68.3%; Pred. No. 1.1e-12; tive 0; Mismatches 54; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AGGIGICCCCAGIGAAGGIGACAGCCCTGGGCGGGGGGAAGIIGGAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Building 30, Room 405, Bethesda, MD 20892
Tel: 3014962111
Fax: 3014020897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yamada@yoda.nidr.nih.gov
Seg primer: AACAAAAGCTGGAGCTCCACC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the rat incisor
J. Dent. Res. 74, 307-312 (1995)
95181657
                                                                                                                      BACKWARD: GTTTCCCAGTCACGACG
Plate: 76 row: C column: 21
Seq primer: ATTRAGGTGACACTARAG.
Location/Qualifiers
1. 337
                                                                                             FORWARD: AGGAAACAGCTATGACCAT
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R47029.1 GI:807371
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NOT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comparation (17) Strausberg, Ph.D. Bmail: cgapber Strausberg, Ph.D. Bmail: cgapber Famail.ini.gov This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                           udlodog.rl scares NMPu Mus musculus cDNA clone TMAGE:1434737 5' similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN: ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 GACTITICCGGAGGACAGAGGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCTGGGC 218
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   204 GITTTCCCTGTGAGAATAATAGCTCTGGAAGAAGGAGACTTGGAGACC 251
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Seq primer: -25m13 rev? Er from Amersham
Seq primer: -52m3 rev? Er from Amersham
High quality sequence stop: 503.
Location/Qualifiers
1. 519
Corganism="Mus musculus"
(Ab.refe" taxaon;10090"
(clone="TiMAGE:1434737"
(clone_lib="Soares_WMPu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.2%; Score 57.2; DB 9;
Best Local Similarity 55.6%; Pred. No. 0.00098;
Matches 110; Conservative 0; Mismatches 88;
                                                                                                                                                                            mRNA
                                                                                                                                                                    519 bp
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AI877465.1 GI:5551514
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Unpublished (1997)
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AW513637/c
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//tissue_type="head"
//dev_stage="6 days neonate"
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//dev_stage="5115 iste_2: BamHI; cDNA library was
//dev_stage="5115 iste_2: BamHI; cDNA library was
//dev_stage="6 days neonate"
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                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Runan Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
location/qualifiers
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/clone="430417003"
/clone="430417003"
/clone="11b="RIKEN full-length enriched, 6 days neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 GIGGCIGICCIGAAGGCICAGGAAGCCCCGCCAGAIGACCIGGIGGAITACTCIGGGAIC 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1111 | 1 | 1 | 1 | 1 | 1 | 24 GIGGAGACCTGCTCCTCACCATCCTGCTGGGGGCTG 83
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/strain="C57BL/6J"
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 Y. and Hayashizaki, Y

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, Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kouno, H., Kouda, M., Xoya, S., Watsuyama, T., Miyazaki, A., Nowurz, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagami, M., Tagami, M., Takeda, Y., Takeda, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y.

RIKEN HONGE ESTS (Arakawa, T., et al. 2001)

Dupublished (2001)

On Jun 8, 2000 this sequence version replaced gi:8383516.

Contact: Yoshinde Hayashizaki

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Ramail and Sciences Generical Googe (Liken go.jp)

Carninci, P., Shibata, Y., Hayatsu, M., Sugahara, Y., Shibata, K., Itoh

Wellization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. . Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Ilaawa, A.,

Hayashirati, Y., Wonda, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kawa, A.,

Hayashirati, Y., Wonda, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kara, A.,

Riffen intervaled sequence analysis (RISA) system. - 34-format
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayshizaki, Y. Carninci, P., Sugahara, Y. and Hayshizaki, Y. and Hayshizaki, Y. and Hayshizaki, Y. computer-rbased methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Knodo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note---Site_1: Sali, Site_2: Bamil: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primed with a primer [5'
GaGaGaGaGaGGAGGAGGGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/db_xref="taxon:10090"
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BB038765 RIKEN full-length enriched, 6 days neonate head Mus
musculus cDNA clone 5430417003 3', mRNA sequence.
BB028765 GI:16258092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor dene Index
Tumor dene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nlh.gov
Trasus Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Rashington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
image.llnl.gov/image/html/iresources.shtml
                  AWE13637

S12 bp mRNA linear EST 03-VAR-2000
S247N10-X1 NCL_CGAP_UT1 Home sapiens CDNA clone HAGE:2707171 3
SIMilar to TR:063613 065813 ODORAWF-BINDING PROTEIN: ; mRNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 626)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11586-014*
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (base; 1 to 52) NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NGT-CGAP interitute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 CGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="haxon:9606"
/db_cref="Taxon:9606"
/dlone="IMAGE:270711"
/dlone_lib="Woll-GGAP_Utl"
/tissue_type="Well-differentiated endometrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51.8; DB 10; Length 532;
Pred. No. 0.019;
0; Mismatches 12; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40UP from calculation quality sequence stop: 316.
Location/Qualifiers
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AW513637.1 GI:7151715
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Best Local Similarity 83.1%;
Matches 59; Conservative
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                                                                                                                                                                      EST 25-MAY-2000
                                                                                                                                                                 AM920286 594 bp mRNA linear EST 25-MAY-2000 EST351590 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIGT45 5' end, mRNA sequence. AM9202086 AM920286.1 GI:8086095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //iissue_type="mix - brain, ovary, placenta, kidney, lung, liver, embryo, heart, muscle, spleen"
//lab.host="SOLR"
//note="Woctor: pBlueScript SK(-); Site_1: EcoR1; Site_2:
//note="Woctor: pBlueScript SK(-); Site_1: EcoR1; Site_2: List Stimated insert size approx: kb"
                                                                                                                                                                                                                                                                                                                Norway rat.
Ratlus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamwalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 594)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Rat gene index, normalized rat, norvegicus, Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 CCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGA---GGCCCAGGAAGGTGTCCCCAG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nhiee@tigr.org
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information
Seq primer: Mi3 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.6%; Score 41.6; DB 10; Length 594; illarity 57.4%; Pred. No. 5.3; Conservative 0; Mismatches 74; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Octobrished (1998)
Contact: Lee, MH
Contact: Lee, MH
Contact: Lee, MH
1712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-888-5529
Tes: (301)-838-529
          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .594

^Organism="Rattus norvegicus"

/db_xref="taxon:10116"

/clone="RGIGT45"
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Best Local Similarity
Matches 124; Conserv
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(Dasses 1 to 660)

(Dasses 1 to 660)

(Pijiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Matanabe, H. and Sakaki, Y.

Direct Submission

Direct Submission

Submitted (02-MG-2001) Asso Fujiyama, The Institute of Physical

submitted (02-MG-2001) Asso Fujiyama, The Institute of Physical

sud Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou, Tsurumi-Ku, Tokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:R1-45-503-911, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end

was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-068L11.R.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGO75726 660 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-068L11.R, genomic survey sequence.
AGO75726
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3'], cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                    66 CCCAGTCACAAGATACCCAGTATAGTTTCCCTGTGAGAATAATAGTCTCTGGAAGAAGA 125
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                                                                                                                                                                                                                                                                                                                                          165 CCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG 224
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                           6 GACCIGGIGGATIACICIGGGATCIGGIACGCAAAGGCCAIGGIACACAAIGGIACCIA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Matanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                      21.4%; Score 50.4; DB 10; Length 626; ilarity 61.4%; Pred. No. 0.043; Conservative 0; Mismatches 51; Indels 0;
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/clone_lib="PTB Chimpanzee Male BAC Library"
215 c 188 g 118 t 1 others
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="ppg-068111.R"
/sex="male"
                                                                                           143 t
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R.Site 1 : SacI
R.Site 2 : SacI.
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LIBRARY
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                                                                                           156 c
                                                                        BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                  225 AAGTIGGAAGCC 236
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                                                                                                                                                                                   Local Similarity
les 81; Conserv
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LOCUS

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[ (bases 1 to 512) Cookers of the Cookers of the Cookers of the Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre of P., Mobermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Wodel, Noicellular System for Analyzing Gene Function and Regulation in Upspublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOB21423 512 bp mRNA linear EST 01-AUG-2002
1030092B09.yl C. reinhardtii CC-1690, Deflagellation (normalized),
Lambda Zap II Chlamydomonas reinhardtii CDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                         CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIALL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://inage.lnll.igov
Plate: LLCAH.446 row: i column: 06
High quality sequence stop: 507.
I. 955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 GIGAAGGCCAIGGIGGICGAIAAGGACIITCCGGAGGACAGGAGGGCCCAGGAAGGIGICC 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 12; Length 955;
Pred. No. 8.5;
0; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTGGAIGITGATCACGGTGGACCTTGGAAGGATGG 185
                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone_lib="NIH_MGC_59"
Amail: cgapbs-r@mail.nih.gov
Pissue Procurement: ATCC
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BQ821423.1 GI:22072085
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Best Local Similarity 49.3%;
Matches 107; Conservative C
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BQ821423
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                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db.xref="t-son:9606"
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/clone=11p="ITI_FL013_FBrn1"
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/lab_host="DH10B"
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602537121F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4656077 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 955)
NIH-WGC http://mgc.nci.nih.gov/.
NIH-WGC http://mgc.nci.nih.gov/.
Ontpiblished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 753)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length Charles and normalization
Unpublished (2001)
AL567433 INT_FL013_FBrn1 Homo sapiens cDNA clone CSODF024YD02 3 prime, mRNA sequence.
AL567433 GI:12920788
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Genoscope - Centre National de Sequencage
BP 191 9106 EVRZ cedex - France
Email: segrefégenoscope.cns.fr. Web : www.genoscope.cns.fr.
1. 753
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BG493366
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Anotes "Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: Xho1; This library, constructed by John Davies and Jeffrey McDermott, comblose Sonsa from C-1690 cells grown to mid-log plase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. Polya mank was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratageme) in the EcoRI (5') and Xho1 (3') sites. PBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratageme) phage. The library was normalized using method 4 described in Bonalde et al (1996) Genome Research 6: 791-806."
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Eukaryota, Viridiplantaeti
Eukaryota, Viridiplantaeti
Chlamydomonas.
Chlamydomonas.

Di (Dases I to 627)

SG Grossman A. Davies; Chlamydomonas.

McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Onicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Onpublished (2000)

AL Onicellular System for Analyzing Gene Function and Regulation in
Vascular Blizabeth H. Harriss
DOMB Exx 91000

Duke University
Durham, NC 27708-1000, USA
Fel: 919 613 8164
Fex: 919 613 8164
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BE212139 1 GI:8828409
                                                                                                  1..597
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, lambda Zap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 597;
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Best Local Similarity 50.0%; Pred. No. 20;
Matches 98; Conservative 0; Mismatches 98;
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers
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/db.ref="taxon:3055"
/db.ref="taxon:3055"
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/clone_lib="taxon: reinhardtii CC-1690, Deflagellation
/note="vector: ppluescript II SK-; Site_I: ECORI; Site_2:
Nho.: Deflagellation library, constructed by John Davies
and Jeffrey MoDermoch, combines connas from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by ph shock. PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRi (5') and XnORI (3') sites
pBluescript II SK- plasmids were excised from the lambda
Zap clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaccae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTCAC 100
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Pred. No. 19;
0; Mismatches 98; Indels
                 Contact: Charles Hauser
DOMB Box 91000
Duka University
Durhau, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Email: chauser@duke.edu.
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BE337290.1 GI:9210375
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Matches 98; Conservative
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Anote-"Vector: pBluescript II SK-; Site_1: BCORI; Site_2:
XhoI; This library, constructed by John Davies and Joffrey
KNDErmott, combines constructed by John Davies and Joffrey
MADERmott, combines constructed by John Davies and Joffrey
and-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POLYA mENA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
AAP II (Stratagene) in the BCORI (5') and XhoI (3') sites
pBluescript II SK- plasmids were excised from the lambda
AAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonalde et al (1996) Genome Research 6: 791-806."
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/strain="CC-1690 wild type mt+ 21gr"
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Chlamydomonas reinhardtii
Eukaryototi Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadecaes; Chlamydomonas.
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Pred. No. 20;
0; Mismatches 98; Indels 0;
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Location/Qualifiers
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Contact: Charles Rauser
DOMB Dox 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Best Local Similarity 50.0%;
Matches 98; Conservative 0
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XhoI; This library, constructed by John Davies and Jeffrey
MoDermott, combines const from C-1690 cells grown to
mid-log phase in TaP (acetate-containing) medium in the
light, TaP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POlyA mRNW was purified from each sample, pooled and cDNA
synthesized. The CDNA was directionally cloned into Lambda
ZAP II (Stratagene) in the ECORI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exhasiset (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) denome Research 6: 791-806."
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                                                                      /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Chlamydowonadaceae; Chlamydowonas.
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Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtil Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
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Durham, NC 27708-1000, USA
Durham, NC 27708-1000, USA
Fax: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers
1. 629
/organism="Chlamydomonas reinhardtii"
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Unpublished (2000)
Contact: Blizabeth H. Harris
DCMB Box 91000
                                       Location/Qualifiers
1. .627
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(normalized), Lambda Zap II"

/note=Vector: pBluescript II Sr.; Site_I: BCORI; Site_2:
Xno1; Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines CDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mRNA was
purified from each sample, pooled and CDNA synthesized.
The CDNA was directionally cloned into lambda Zap II
(Stratagene) in the ECORI (5') and XNORI (3') sites.
PBluescript II SK- plasmids were excised from the lambda
Zap clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
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BASE COUNT 122 a

Query Match
16.6%; Score 39.2; DB 14; Length 645;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps

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364 GCICAAAGAAGAAGAAGAAGATGGGTGTGCTGCGCCAGCGAGAAGATGGCGCAGCTGAA 423

8

QY 221 TGGGAAGTTGGAAGCC 236

Search completed: February 10, 2003, 04:57:54 Job time : 670.018 secs

Title: Perfect score:

Run on:

Sequence:

Scoring table:

X62418 H.sapiens m X62418 H.sapiens m X67647 H.sapiens m M90424 Human tear X52016 F.norvegitu AF027177 Canis fam AR070057 Sequence linear PAT 20-JUN-2002 X74806 R.norvegicu S77587 VEG protein AJ251023 Homo sapi M76734 Rat odorant BC027556 Mus muscu AC125365 Rattus no X15213 Tammar wall AC121473 Rattus no AR204078 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description Unknown.
M Unknown.
M Unknown.
M Chaseslited.
E 1 (Dasesl to 522)
S Conklin,D.C.
Antibodies to lipocalin homologs
AAL Patent: US 6365716-A 1 02-APR-2002;
Location/Qualifiers DNA AR204078 522 bp Sequence 1 from patent US 6365716. AR204078 AR204078.1 GI:21500632 SUMMARIES RATTY2G12A BC027556 AX204078 AX451327 AX083544 rvu34287 RNVEGP 22 8 42.5 39.3 31.0 Query Match Length Unknown. Score 245 245 245 245 245 240.2 240.2 240.2 240.2 240.2 181 136.6 136.6 136.6 136.6 136.6 136.6 105.8 104.2 104.2 96.2 83.6 DEFINITION ACCESSION VERSION KEYWORDS ORGANISM RESULT 1 AR204078 SOURCE Result (without alignments) 8933.518 Million cell updates/sec February 9, 2003, 22:02:40 ; Search time 798.139 Seconds US-09-099-823-2 245 1 GGATATCACAGGGACCTGGT......CATGTACCTGCAGGAGCTGC 245 4109280 GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_htg_inv:* em_htg_other:* em_htg_mus:*
em_htg_pln:*
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gb_pl:* gb_sy:* gb_un:* gb_vi:* em_mu:* em_om:* em_or:* em_in:* em un: em_ro: GenEmbl:*

Database :

REFERENCE AUTHORS TITLE JOURNAL FEATURES

No. is the number of results predicted by chance to have a

Pred.

em_htgo_other:*

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Homo sapi Sequence

121 AGCCACGITCACCITCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGGAA 180

PAT 28-FEB-2001

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1 (bases 1 to 676)

Pitito, G., Lacasette, E. and Gachon, F. odorant-binding human profesins fixing hydrophobic ligands:

polypeptides and polynucleotides coding for said polypeptides and sess thereof
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Patent: WO 0112806-A 9 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 676
/organism="Homo saplens"
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43. 555
/note="conA2098 (676) - forme classique (hOBPlIb-alpha)"
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/db_xref="G1:21698380"
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REPREDHYIFYCKDQHHGGLLHMGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Use of human phermone polypeptides
Patent: WO 0223201-A 1 21-MAR-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
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/organism="unknown"
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      PAT 06-JUL-2002
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Goddwski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,E., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye.N.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                      Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
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  739 bp I
Sequence 205 from Patent WO0208284.
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AX454620.1 GI:21713934
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207 c 205 g 117
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Lacazette, E., Gachon, M., and Pitiot, C. A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934; differential expression in the oral and genital spheres
10075326
                                      HSA251026
Homo sapiens mRNA for putative odorant binding protein b-a (OBFILD
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2 (bases 1 to 676)
Gacdon, A.M.
Direct Submission
Submitted (26-0CT-1999) Laboratoire de Biochimie Medicale - INSERM U384, Universite d'Auvergne - Raculte de Medecine, 28, place Henri Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
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AJ251026.1 GI:6900076
AJ251026.1 GI:6900076
OBPILD gene; odorant binding protein.
Homo sapiens.
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43. .555
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/translation='mktiricytiglaaalsftleeditgywyykanyydxdfpedr
rprkyspykytalgggnleatftrmedrciokkilarkteepgkrsayggrkliylo
blegtddyybycychoorrgglrymsklygrnentnlealeefkklyghkglsbedifmp
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Homo sapiiens mRNA for putative odorant biding protein aa (OBPIIa
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1 (bases 1 to 676)

Lacacette, F., Gachon, A.M. and Pitiot, G.
A novel human adorant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
                                                                                                                                                        181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                            61 CAGGAGGCCCAGGAAGGIGTCCCCAGTGAAGGIGACAGCCCTGGGCGGTGGGAAGTIGGA 120
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                    1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA
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7/gene="control of the control of t
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AJ51021.1 G1:6900066
OBPIIA gane; odorant binding protein.
Homo sapiens.
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Matches 242; Conservative
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/db_xref="G1:13185347"
/translation="MKTPLGYTGGLAAALSFTLEEEDITGTWYVXAMVVDKDFPEDR
PRENYSPYKYTALGGGNLEAFPTPREDROIGKTLARKTEEPGRESAYGGRULITLO
ELPGTDDYVFYCKDQRRGGLRYMGKLYGRNPYTNLEALEEFKKLYQHKGLSEEDIFMP
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1 (bases 1 to 676)
Pitiot, G., Lacazette, E. and Gachon, F. Odorant-binding human proteins fixing hydrophobic ligands: polypeptides and polynucleotides coding for said polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACACACCCTGGGCGGTGGGAAGTTGGA 120
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Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis Patent: WO 0200690-A 205 03-JAN-2002; Genentech, Inc. (US) Location/Qualifiers
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                                                                                                                                                                                                                                                                                            Length 739;
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/note="cDNA396 (676) /g1 (hOBPIIa-alpha)"
/codon_start=1
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Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 676
/Organism="Homo sapiens"
/Organism="Homo sapiens"
43. .555
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 1 from Patent W00112806.
AX083536 AX083536.1 GI:13185346
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Homo sapiens mRNA for putative odorant binding protein ab (OBFIIa
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1 (bases 1 to 725)

Lacazette, Gachon, A. M. and Pitiot, G.
A novel human odcrant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
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Submitted (26-0-1999) Laboratoire de Biochimie Medicale - INSERM
Submitted (26-0-1999) Laboratoire de Medecine, 28, place Henri
1384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
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Pred. No. 1.18-48;
0; Mismatches 3; Indels 0.
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AJ7551022.1 GI:6900068
OBPIIa gene; odorant binding protein.
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/db_xref="taxon:9606"
/chromosome="9"
/map="9934"
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43. .483
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Best Local Similarity 98.8%;
Matches 242; Conservative
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//protein_id="CAC333233.1"
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Odorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and
uses thereof
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
Pitiot, G., Lacazette, E. and Gachon, F.
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                      61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGGAGTTGGA 120
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1 GGATATCACAGGGACCTGGTACGTGAAGGCCCATGGTGGTCGATAAGGACTTTCCGGAGGA
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Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 725
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/db_xref="taxon:9606"
43. .483
/note="cDNA396 (725) /SM12 (hOBPIIa-beta)"
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Sequence 3 from Patent W00112806.
AX083538 1 GI:13185348
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PWKNLRWMGSYRDSRRYFSGPFRAREAFSNTRQPPFGLHLGSPPYHGTQSPDHIDLPS
SHDPSILPPT"
                                                                                                                                                                                                                                                                                 Direct Submitted (26-007-1999) Laboratoire de Biochimie Medicale - INSERM Direct Submitted (26-007-1999) Laboratoire de Biochimie Medicale - INSERM U384, Directsite d'Auverand e eacol 63001, FRANCE LOCATION, Perrand cedex01 63001, FRANCE | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 | 1.041 
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         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 741)

1 clasact.p.R., Gachon,A.M. and Pitiot,G.
A novel human odcrant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAGGAGGCCCAGGAAGGTGCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
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Sequence 11 from Patent W00112806.
AX083546 AX083546.1 GI:13185356
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AX083546
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db.xref="taxon:9606"
43. 729
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PWRKILRNWCGFRDSRRRFFSCPCRREAAFSNTRQPFGLHLQSPPTHQTGSPDHLDLFS
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[ (bases 1 to 741)

Pittot, G., Lacaette, E. and Gachon, F.

Pittot, G., Lacaette, E. and Gachon, F.

polymetridas and polymucleotides coding for said polypeptides and uses thereof

patent: WO 0112806-A 5 22-FEB-2001;

Universite d'Auvergne (FR); Pitiot, Gilles (FR)

Location/Qualifiers
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AJ251024.1 GI:6900072
BDELTA gene; odorant binding protein.
Homo sapiens.
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Sequence 5 from Patent W00112806.
AX083540 GI:13185350
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TPALWEALAIDTLRKLRIGTRRPRIRWGQEAHVPAGAAQBGPLHLLLQRPAFWGFAPH
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61.6%; Pred. No. 3.4e-34;
ive 52; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                   85.3%; Score 209; DB 9; Length 782; illarity 100.0%; Pred. No. 4.8e-41; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 510)

2 Onklin_D.C.

Antibodies to lipocalin homologs

Antibodies to lipocalin homologs

Antibodies to lipocalin homologs

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Sequence 5 from patent US 6365716.
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43. .340
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Best Local Similarity 61.6%
Matches 151; Conservative
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LILORPAPWGPAPHGKACG"
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Lacazette, E., Gachon, A.M. and Pitiot, G. A. and human odorant-binding protein gene family resulting from genomic duplicons at 9934; differential expression in the oral and
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  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 782) Pititot,G., Lacaette,E. and Gachon,F. odorant-binding human proteins fixing hydrophobic ligands: polypeptides and polyncleotides coding for said polypeptides and sess thereof
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/note="cDNA2098 (782) - forme longue (hOBPIID-beta)"</pre>
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                                                                                                                               Patent: WO 0112806-A 11 22-FEB-2001;
Daiversite d'Auvergne (FR) ; Pitiot, Gilles (FR)
Location/Qualifiers
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Hum. Mol. Genet. 9 (2), 289-301 (2000)
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OBPILD gene, odorant binding protein.
Homo sapiens.
Homo sapiens
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Search completed: February 10, 2003, 03:12:34 Job time : 805.139 secs

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MR, Kratochvil JD;
H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Billing-medel PA, Cohen M, Colpitts TL, Gordon J, Granados EN, Hodges SC, Klass Russell JC, Scheffel CP, Stroupe SD, Yu
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AAVO8842
AALO3258
AALO3257
AAF80047
AAF80046
AAXO7453
  AAC58615
AAA37071
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AAS93598
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AAS87379
AAS77495
AAS79120
AAS70144
                AAA37071
ABL95663
ABL88174
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AAXO7454
ID AAXO7454 standard; cDNA; 245
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    98WO-US12862.
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    WPI; 1999-105623/09.
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  Homo sapiens.
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245
1 GGAIATCACAGGGACCTGGT......CATGTACCTGCAGGAGCTGC
                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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AAX76054
AAS76054
AAX91770
AAX91770
AAX07456
AAX67457
                                                                 - nucleic search, using sw model
                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                 nucleic
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No.
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The present sequence encodes a human lipocalin homologue, designated alipocalin homologue, alipol, is specifically expressed in tests and mammary gland, particularly breast tumour tissue. Based on this tissue distribution, alipol may be used as a diagnostic for breast carcinomas and as a tool for predicting tumour aggressiveness. Aponists can be used for transportation of small hydrophobic molecules either in vivo or in vitro, and so are useful in specifically promoting the growth and/or development of testis-specific call lineages in culture. Zilpol can be used to identify inhibitors. Zilpol proteins can also be used to prepare antibodies (which can be linked to toxins), and can serve as prepare antibodies (which can be linked to toxins), and can serve as immunogens. Zilpol proteins can be used as delivery and encapsulation system to transport and/or stabilise small lipophilic molecules, e.g. to protect from gut pH and digestive enzymes. They can also be used to protect from gut pH and digestive enzymes. They can also be used to protect from gut pH and digestive enzymes. They can also be used to protect from gut pH and digestive enzymes. They can also should be used to bind strikin, e.g. to transport retinoids or steroids to receptors, in the particular as therapy for breast cancer, emphysema and diseases of the skin. They may also play an important role in reproduction. Other uses include anti-inflammatory responses, and antimicrobial activities.

Zipol uncleic acid sequences may be used for gene therapy to increase or inhibit zipol activity, to derive probes and primers, to derive antisense sequences, and to detect genetic abnormalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; lipocalin protein; Zlipol; glycodelin; phermone; anxiety; beneficial mood; hypothalamic; satiety; identification; energy balance; reproductive biology; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GACGGAGGACCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
restricted to testis and mammary gland tissues, particularly breast tumour tissue, used to, e.g. predict tumour aggressiveness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 245; DB 20; Length 522; Best Local Similarity 100.0%; Pred. No. 6.3e-59; Matches 245; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 522 BP; 125 A; 132 C; 172 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
8..517
/*tag= a
                                                                        Claim 3; Page 82-83; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD35179 standard; DNA; 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Zlipol DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GCTGC 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD35179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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breast cancer; emphysema; skin disease; reproduction; anti-inflammatory;
antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACACCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                            treating diseases or conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New lipocalin homologue designated zlipo1 - whose expression is
                                                                                                                                                                                                                                                          wery match 100.0%; Score 245; DB 20; Length 245; Best Local Similarity 100.0%; Pred. No. 5.2e-59; Matches 245; Conservative 0; Mismatches 6. T.
                                                                                                                      The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lipocalin homologue zlipol encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                          Sequence 245 BP; 62 A; 54 C; 89 G; 40 T; 0 other;
          detecting, diagnosing, preventing or
of the breast, such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
7..519
/*tag= a
                                                                              Claim 11; Page 94; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX19505 standard; DNA; 522 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US16425.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9907740-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1999.
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AAX19505
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The invention relates to isolated polynuclectide (I) and conjugetide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome configurerase chain reaction (PGR) primers, oligomers, and for chromosome can gene mapping, and in recombinant production of (II). The configures configures are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for reactor normal activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques con the configuration a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of states expressing (II). (I) and (II) are useful for treating imaging of states expressing (II). (I) and (II) are useful for treating inapprofice adaption expression or biological activity. The polypeptide and polymuclectide sequences have applications in the printed and to produce other types of data and products dependent on DNA and diagnostic coding sequences. Absolyfe4 represent novel human configuration, but was obtained in electronic format directly from WIPO configuration, but was obtained in electronic format directly from WIPO configuration, but was obtained in electronic format directly from WIPO configuration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AGCCACGITCACCITCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 245; DB 23; Length 603; Best Local Similarity 100.0%; Pred. No. 6.6e-59; Matches 245; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 603 BP; 142 A; 178 C; 182 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 11858; 103pp; English.
                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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                                                        WO200175067-A2
                    Homo sapiens
                                                                                                      11-OCT-2001.
δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of using two human lipocalin proteins, Zlipol and glycodelin as phermone polypeptides. Human phermones are used to allevate anxiety, promote beneficial moods and to alter hypothalamic functions, such as satiety, energy balance and reproductive biology. The sequences of the invention are used for identifying the presence of Zlipol neceptor in a test sample, or for identifying the presence of a Zlipol ligand or a glycodelin ligand at est sample. The present sequence is human Zlipol DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGAGA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AGCCACGITCACCITCATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                     Use of zlipol or glycodelin (human pheromone polypeptides) for identifying presence of Zlipol receptor, glycodelin receptor, Zlipol ligand or glycodelin ligand in test sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Opery Match 100.0%; Score 245; DB 24; Length 523; Best Local Similarity 100.0%; Pred. No. 6.4e-59; Matches 245; Conservative 0; Mismatches 0; Indels 0;
/product= "Human Zlipol protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 523 BP; 125 A; 133 C; 172 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #11858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 46-47; 50pp; English.
                                                                                                                                                                                                                                                                                                                 Foster DC, Holloway JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS76054 standard; cDNA; 603 BP.
                                                                                                                                                                           12-SEP-2001; 2001WO-US28525.
                                                                                                                                                                                                                            13-SEP-2000; 2000US-232218P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                              /partial
                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-362374/39.
P-PSDB; AAE22099.
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                                                                                            WO200223201-A2
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                                                                                                                                                                                                                                                                                                                                                                           Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia, obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "odorant binding polypeptide OBPIIb-alpha"
                                                                                                                                                                                                                                                                                                       Nucleotide sequence of odorant binding polypeptide OBPIIb-alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 113-114; 132pp; French.
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43..555
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                                                                       AAF80043 standard; cDNA; 676 BP.
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                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYAU-) UNIV AUVERGNE. (PITL/) PITIOT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-202864/20.
P-PSDB; AAB67742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          release of perfumes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200112806-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                   AAF80043;
RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      imaging
                    231 AGCACGTICACCIICATGAGGGAGGAICGGIGCAICCAGAAGAAAAICCIGAIGCGGAA 290
CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                    121 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                                                                     181 GACGGAGCGAGCCTGGCAAATACAGCGCCTATGGGGGCGCAGGAAGCTCATGTACCTGCAGGA 240
                                                                                                                                                             Human, breast specific gene, breast specific marker, BSG; diagnosis; breast cancer, therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific genes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGATATCACAGGGACCTGGTACGTGAAGGCCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 690 BP; 161 A; 208 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast specific gene LS clone 1213903.
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                                                                                                                                                                                                                                                                                                                                  AAZ91770 standard; DNA; 690 BP.
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                                                                                                                                                                                                           241 GCTGC 245
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                                                                                                                                                                                                                                            351 GCTGC 355
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121 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                 181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                                                    193 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAGGTCATGTACCTGCAGGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AGCCACGTTCACCTTCATGAGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated BS124 polynucleotides and polypeptides - used for detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
                                                                                                                                                                                                                                                                                                                     BS124; breast; cancer; detection; diagnosis; prevention; treatment; consensus; EST; ss.
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Gordon J, Grandos EN, Hodges SC, Klass MR, Kratochvil JD;
Kussell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 245; DB 20; Length 692; Best Local Similarity 100.0%; Pred. No. 6.8e-59; Matches 245; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a consensus BS124-specific EST clone. It is useful for detecting, diagnosing, stading, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                             Human BS124 specific BST clone consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 95; 125pp; English.
                                                                                                                                                                                                            AAX07457 standard; cDNA; 692 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US12862.
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                                                                                                                                                                                                                                                                  08-JUN-1999 (first entry)
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                                                                                                               241 GCTGC 245
                                                                                                                                  . 353 GCTGC 357
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                       AAX07457;
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                                                                                                               113 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTGGTGGTAAGGACTTTCCGGAGGA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated BS124 polynucleotides and polypeptides - used for detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 BS124; breast; cancer; detection; diagnosis; prevention; treatment;
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Granados EN, Hodges SC, Klass MR, Kratochvil JD;
, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 245; DB 20; Length 692; Best Local Similarity 100.0%; Pred. No. 6.8e-59; Matches 245; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      Human BS124 specific EST clone 1730294IH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Pages 94-95; 125pp; English.
                                                                                                                                                                                                                                                                       AAX07456 standard; cDNA; 692 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US12862.
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                                                                                                                                                                                           353 GCTGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                             08-JUN-1999
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Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998
                                                                                                                                                                                                                                                                                                  AAX07456;
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Human; immune related disease; diagnosis; antiinflammatory; cardiant, dermatological; antiarthritic; autirheumatic; immunosuppressive; dermatological; antiarthritic; autifiabetic; notropic; neuroprotective; mitianeemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatord arthritis; softeoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; diopathic inflammatory myopathy; Sjogran's syndrome; thyrodidits; systemic vasculitis; autoimmune haemolytic anaemia; diabates mellitus; dutoimmune thrombocytopaenia; immune-mediated renal disease; undiamatory bowel disease; pheptobiliary disease; Whipple's disease; inflammatory bowel disease; income mediated skin disease; allergic disease; autoimmune disease; immune-mediated skin disease; allergic disease; wimmunological disease; immune-mediated skin disease; allergic disease; kw graft rejection; graft-versus-host-disease; ss.
CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGAAGTTGGA 120
            121 AGCCACGTTCACCTTCATGAGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                    181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCCAGGAAGCTCATGTACCTGCAGGA 240
                                                                                                                      293 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 352
                                                                                                                                                                                                                                                                                                                                              Human PR01283 protein UNQ653 encoding cDNA SEQ ID NO:169.
                                                                                                                                                                                                                                                               AAC58615 standard; cDNA; 739 BP.
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99US-0131445.
99US-0132371.
99US-0134287.
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9908-0141037.
9908-0144758.
9908-0146528.
9908-014622.
9990-0520594.
9990-0521090.
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99US-0123618.
99US-0123957.
99US-0125775.
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                                                                                                                                                                                                                                                                                                                       29-JAN-2001 (first entry)
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                                                                                                                                                                  241 GCTGC 245
                                                                                                                                                                                            353 GCTGC 357
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04-MAY-1999;
14-MAY-1999;
02-JUN-1999;
23-JUN-1999;
26-JUL-1999;
28-JUL-1999;
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13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
Wattanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or Knockout animals which are in turn useful for development and secreening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
 100.0%; Score 245; DB 22; Length 738;
ilarity 100.0%; Pred. No. 6.9e-59;
Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
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                                                                                                                                                                                                                                     DNA encoding protein of the invention #50.
                                                                                                                                                                                                                                                                  Secreted; transmembrane; gene therapy; ss.
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                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1999; 990S-01441037.
26-JUL-1999; 990S-0144738.
26-JUL-1999; 990S-0145698.
01-SEP-1999; 990S-0162506.
30-NOV-1999; 990V-0528313.
02-DEC-1999; 990O-0528313.
05-JAN-2000; 2000MO-US00379.
                                                                                                                                                     AAF54313 standard; DNA; 738
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                                                                                                                                                                                                          02-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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                                                         241 GCTGC 245
                                                                            353 GCTGC 357
                                                                                                                                                                                                                                                                                             Unidentified.
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Matches 245;
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Human, PRO polypeptide, membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
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                                                                                                                                                                                                            AAA37071 standard; cDNA; 739 BP.
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98US-0098749.
98US-0098873.
98US-0098821.
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98US-0099536.
98US-0099596.
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98US-0101068.
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                             241 GCTGC 245
                                                                            353 GCTGC 357
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16-SEP-1998;
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17-SEP-1998;
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                                                                                                                                                                                                                                                           AAA37071;
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ID AAAA37071

ID AAAA37071

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rhewmatoid arthritis, osteoarthitis, thyroiditis and diaberes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
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30-NOV-1999; 99W0-US28409.
01-DEC-1999; 99W0-US28634.
02-DEC-1999; 99W0-US28654.
02-DEC-1999; 99W0-US28564.
02-DEC-1999; 99W0-US28566.
02-DEC-1999; 99W0-US28566.
02-DEC-1999; 99W0-US28566.
03-DEC-1999; 99W0-US28565.
05-TAN-2000; 2000W0-US00219.
06-TAN-2000; 2000W0-US00217.
06-TAN-2000; 2000W0-US00376.
11-PEB-2000; 2000W0-US03565.
11-PEB-2000; 2000W0-US03565.
11-PEB-2000; 2000W0-US03565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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Human, anglogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy, endothelial disorder; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
                                                                                                                                                                                                                                                Analy22 to Analy144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in Any99340 to Any99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand intractions. The polypeptides and nucleotide sequences encoding them have various industrial applications, including uses as pharmaceutical and diagnostic agents. Analy3145 to Analy330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                  New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
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                                                                                              Smith V, Watanabe CK,
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                                                                                                 Gurney AL,
                                                                                                                                                                                                                         Claim 2; Fig 99; 773pp; English.
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98US-0108851.
98US-0108852.
98US-0108858.
98US-0108904.
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                                                                     (GETH ) GENENTECH INC.
                                                                                                 Baker K, Goddard A,
                                                                                                                         WPI; 2000-237871/20.
P-PSDB; AAY99389.
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 18-NOV-1998;
18-NOV-1998;
18-NOV-1998;
18-NOV-1998;
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 9805-0101479.
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9805-0102337.
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98US-0103711
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    23. SERP-1998;
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The present invention provides the protein and coding sequences of human pro proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angingenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
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                                                                                                                                                                                                                                                                                                Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
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2000US-219556P.
2000US-220624P.
2000US-220664P.
2000WO-US20710.
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2000005-064367.
200000-0523522.
200000-0523328.
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ABL88174
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Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
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2000WO-US30952.
2000WO-US30873.
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GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
GURNEY A I.
HILLAN K J.
MARSTERS S A.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
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P-PSDB; ABB95525.
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FERRARA N.
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23-AUG-2000; 2
24-AUG-2000; 2
07-28P-2000; 2
118-SEP-2000; 2
14-CCT-2000; 2
24-CCT-2000; 2
08-NOY-2000; 2
10-NOY-2000; 2
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25-JUL-2000;
25-JUL-2000;
28-JUL-2000;
02-AUG-2000;
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(WOOD/)
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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPIII-alpha OBPS provide long-term retention (gradual clease) of lipophilic compounds, so prolong the 'hold' of perfumes, relacions of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly) as competitive inhibitors (c) (agonists or antagonists) of cellular lipopalcin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for confrolling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in dorant for treating hyperlipidemia or obesity, or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as a cransporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or comparation of the foetus; as a marker of pregnancy or milallergic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma, cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
                            181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                                      293 GACGGAGGACCTGGCAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACTGCAGGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "odorant binding polypeptide OBPIIa-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of odorant binding polypeptide OBPIIa-alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 106-107; 132pp; French.
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43..555
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                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-2001 (first entry)
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P-PSDB; AAB67738.
                                                                                                                             241 GCTGC 245
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                                                                                                                                                                       353 GCTGC 357
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AAF80039
ID AAF8
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The PRO proteins and polynoleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiatreriosclerotic
antiangiogenic, hypotensive, vulnerary and antiatreriosclerotic
activities, and can be used in gene therapy. The PRO polynoclectides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endochelial or angiogenic disorder in a mammal,
confider hypertrophy, traum, cancer, age-related medular
degeneration, atherosclerosis, hypertension, arterial restenosis,
lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
carcinoma) and wound healing. The PRO polynoclectides have applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping, ABL88259 to ABL88257 represent primers and
probes used in the exemplification of the present invention.
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Godowski PJ, Gurney AL, Hilllan KJ, Marsters SA, Pan J, Paoni NP;
Stephan JF, Metradbe CK, Milliams PM, Wood WI, Ye W;
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Best Local Similarity 100.0%; Pred. No. 7e-59;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothellal or angiogenic disorders in a mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 205; 565pp; English.
18-SEP-2000, 2000US-0664610.

18-SEP-2000, 2000US-065350.

24-CCT-2000, 2000US-024922P.

08-NOY-2000, 2000US-0759238.

10-NOY-2000, 2000WS-0739673.

10-NOY-2000, 2000WS-0739673.

20-DEC-2000, 2000WS-0732678.

20-DEC-2000, 2000WS-0732678.

21-MA-2010, 2001US-076769.

28-FEB-2001, 2001US-076769.

28-FEB-2001, 2001US-07666.

10-MAR-2011, 2001US-086689.

22-MAR-2001, 2001US-086689.

14-MAR-2011, 2001US-086689.

10-MAR-2011, 2001US-0866034.

25-MAR-2001, 2001US-0866028.

25-MAR-2001, 2001US-0866034.

25-MAR-2001, 2001US-0866034.
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P-PSDB; ABB84919.
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Score 240.2; DB 22; Length 725; Pred. No. 1.5e-57; 0; Mismatches 3; Indels 0;

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hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect specific antiboddes for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, controlling volatilisation of an odorant, specifically in perfumes, occurrently of allergy actions of a specifically of controlling volatilisation of an odorant, specifically in perfumes, controlling of antipopations, e.g. human pheromones, for binding to OBP, also in for treating hyperipidamia or obseity, or to supplement non-maternal controlling pheripidamia or obseity, as to dead additives; as a controlling and as a controlling pheripidamia or of the foetus; as a marker of pregnancy or controlling pheripidamia or of the foetus; as a marker of pregnancy or controlling pheripidamia or of the amniotic membrane; and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AGCCACGITCACCITCAIGAGGGAGGAICGGIGCAICCAGAAGAAAAICCIGAIGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
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Best Local Similarity 98.8%;
Matches 242; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiallergic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes -
                                                                                                                                                                                                                                                                                                                                                                                                                            GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                                                                                                                                                                                                                                                        61 CAGGAGGCCCAGGAAGGIGTCCCCCAGIGAAGGIGACAGCCCIGGGCGGIGGGAAGIIGGA 120
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4.7424 - Artage - Ar
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                                                                 Score 240.2; DB 22; Length 676;
Pred. No. 1.5e-57;
0; Mismatches 3; Indels 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF80040 standard; cDNA; 725 BP.
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                                                                              Query Match 98.0%;
Best Local Similarity 98.8%;
Matches 242; Conservative
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(PITI/) PITIOT G.
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P-PSDB; AAB67739.
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110, Appl
5, Appl
6, Appl
20, Appl
21, Appl
21, Appl
11, Appl
12, Appl
14, Appl
14, Appl
16, Appl
17, 
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    sequence 5 sequence 6 sequence 6 sequence 6 sequence 6 sequence 2 sequence 2 sequence 1 sequence 1 sequence 5 sequence 5 sequence 5 sequence 6 
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        US-09-085-199B-10
US-09-227-357-98
US-08-813-150-5
US-08-869-669-20
US-08-869-669-21
US-08-869-669-21
US-08-869-677-1
US-08-869-677-1
US-08-869-677-1
US-08-86-977-1
US-08-86-977-1
US-08-86-977-1
US-08-86-977-1
US-08-86-977-1
US-08-105-171-74
US-08-105-571-74
US-08-105-571-74
US-09-105-571-74
US-09-105-571-74
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US-09-105-571-74
US-09-105-571-74
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Patent No. 6020163
Patent No. 6020163
Patent No. 6020163
Patent No. 1020163
Patent No. 1020164
Patent No. 1020164
Patent No. 1020164
Patent Patent No. 11002164
Patent Patent Patent No. 10201730, 663A
CURRENT PAPLICATION NUMBER: US/09/130, 663A
CURRENT PATING DATE: 1998-08-05
PARLIER PATING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SEGTUARE: PateSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH 522
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ORGANISM: Homo sapiens
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; LOCATION: (7)...(516)
US-09-130-663-1
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US-09-432-335-1
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Sequence
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245
1 GGATATCACAGGGACCTGGT......CATGTACCTGCAGGAGCTGC
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:: /cgn2_6/ptodata/l/ina/5A_COMB.seq:*
:: /cgn2_6/ptodata/l/ina/6B_COMB.seq:*
:: /cgn2_6/ptodata/l/ina/6A_COMB.seq:*
:: /cgn2_6/ptodata/l/ina/6B_COMB.seq:*
:: /cgn2_6/ptodata/l/ina/B_COMB.seq:*
:: /cgn2_6/ptodata/l/ina/packfiles1.seq:*
                                                              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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8 US-09-614-022-1

8 US-09-614-022-1

8 US-09-432-335-1

8 US-09-432-335-5

8 US-08-467-603-1

8 US-08-467-603-1

8 US-08-467-603-1

8 US-08-467-603-1

8 US-09-130-663-24

8 US-09-130-663-24

8 US-09-130-663-15

8 US-08-133-15

8 US-08-133-15

8 US-08-133-15

8 US-08-133-15

8 US-09-130-614

8 US-08-133-15

8 US-09-130-614

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8 US-09-130-133-133-13

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                 nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                 61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                         121 AGCCACGTTCACCTTCATGAGGAGGATGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                   181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAAGGAAGCTCATGTACCTGCAGGA 240
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                                                                                                                  1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
                                                                                          1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
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OTHER INFORMATION: Degenerate sequence derived from human zlipol
OTHER INFORMATION: nucleotide sequence
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                                               o;
Length 522;
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Query Match 100.0%; Score 245; DB 4; Length 52 Best Local Similarity 100.0%; Pred. No. 4.5e-59; Matches 245; Conservative 0; Mismatches 0; Indels
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APPLICATE CONTINIA, DATE-LI C.
APPLICATE CONTINIA, DATE-LI C.
TITLE OF INVENTION: LIPPOCALIN HOWOLOG;
FILE REPERRNCE: 97-24
CURRENT APPLICATION WUMBER: US/09/130,663A
CURRENT FILLING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILLING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KET: variation
) LOCATION: (1)...(510)
) CTHER INFORMATION: n is any nucleotide
US-09-130-663-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09130663A Patent No. 6020163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GCTGC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 GCTGC 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 245; DB 3; Length 52 Best Local Similarity 100.0%; Pred. No. 4.5e-59; Matches 245; Conservative 0; Mismatches 0; Indels
Sequence 1, Application US/09432335
Patent No. 6143720
GENERAL INFORMATION:
FILE PETERENCE: 97-24
CURRENT APPLICATION ILPOCALIN HOMOLOG
FILE PETERENCE: 197-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
BARLIER APPLICATION NUMBER: 09/130,663
FRALLIER APPLICATION NUMBER: 60/054,867
FRALLIER APPLICATION NUMBER: 60/054,867
SARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE FILING DATE: 1997-08-06
SOFTWARE TELING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CORKIN, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/614,022
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ. ID NOS: 30
SOFTWARE: PRSEED fOR WINGONS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09614022
Patent No. 6365716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (7)...(516)
US-09-432-335-1
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; LOCATION: (7)...(516)
US-09-614-022-1
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US-09-614-022-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
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189 RGCNACNTIYACNTIYATGMGNGARGAYMGNTGYATHCARAARAARATHYTNATGMGNAA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAGGAGGCCCAGGAAGGIGTCCCCAGTGAAGGIGACAGCCCTGGGCGGTGGGAAGTIGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCCAGGAAGCTCATGTACCTGCAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 RACNGARGARCCNGGNAARTATWSNGCNTAYGGNGGNMGNAARTTNATGTAYYTNCARGA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGATATCACAGGGACCTGGTACGTGAAGGCCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
                                                                                                                                                                                                                                                                 OTHER INFORMATION: Degenerate sequence derived from human zlipol OTHER INFORMATION: nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.9%; Score 181; DB 4; Length 510; Best Local Similarity 61.6%; Pred. No. 2.28-41; Maketches 151; Conservative 52; Mismatches 42; Indels
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APPLICANT: Kanleczny, Andrzey
APPLICANT: Braincaukas, Christine B.
APPLICANT: Brauer, Andrew W.
APPLICANT: Brauer, Andrew W.
APPLICANT: Brauer, Andrew W.
APPLICANT: Brauer, Andrew W.
APPLICANT: BRAINCON: Allegenic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: variation
; LOCATION: (1)...(510)
; OTHER INFORMATION: n is any nucleotide
US-09-614-022-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
WEDIUM TYPE: FLOPPY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: APPLICATION NUMBER: 07/999,712
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Patent No. 5843672
GENERAL INFORMATION:
                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-Dec-92 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASCII-text
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STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GCTGC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 RYTNC 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                      Q ID NO 5
LENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-467-603-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                   US-09-432-335-5
Sequence 5, Application US/09432335
Patent No. 6143720
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: LIPOCALIN HOWOLOG;
FILE REFERENCE: 97-24
CURRENT PAPLICATION NUMBER: US/09/432,335
CURRENT PILING DATE: 1999-11-02
BEALIER PAPLICATION NUMBER: 06/130,663
BEALIER PILING DATE: 1999-09-06
BEALIER PILING DATE: 1997-08-06
NUMBER OF SER ID NOS: 30
SOFTHARE: FRASEER OF IN MINIORS VERSION 3.0
SER ID NO 5
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US-09-614-022-5
US-09-614-022-5
Sequence 5, Application US/09614022
Fatent No. 6365716
FATELE THORMATION:
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT FILING DATE: 2000-07-11
FRIOR APPLICATION NUMBER: 09/130,663
PRIOR APPLICATION NUMBER: 09/130,663
PRIOR PILING DATE: 1998-08-06
FRIOR FILING DATE: 1999-08-06
FRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
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NAME/KEY: variation
LOCATION: (1)...(510)
CITER INFORMATION: n is any nucleotide
US-09-432-335-5
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                               309 RYTNC 313
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309 RYTNC 313
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TYPE: DNA

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61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
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Sequence 1, Sapalication US/08491861A

Parent No. 5339283

Sequence 1, Sapalication US/08491861A

Parent No. 5339283

APPLICANT: Morganistern, Jay P.
APPLICANT: Morganistern, Jay P.
APPLICANT: Morganistern, Modraw W.
TITLE OF INVENTION: Allengemic Proteins and Peptides from Dog TITLE OF INVENTION: Dander and Uses Therefor NUMBER OF ENQUENCES: 104

CORRESPONDENCE ADDRESS: 104

CORRESPONDENCE ADDRESS: COCKFIELD, LLP

STREET: Boston

CITY: Boston

STATE: MA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%; Score 70.4; DB 2; Length 525; 59.2%; Pred. No. 7.9e-11; Live 0; Mismatches 91; Indels
                                                                                                                                                                                                                                    IMI-026CP(IPC-048CP)
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/491,861A
FILING DATE: 27-OCT-1995
                                                         07/999,712
            FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY, AGENT INFORMATION:
NAME: Mandragoures, Amy E.
REGISTRATION NUMBER: 56,207
FRETERRENE/COCKET NUMBER: IMI-08
TELEPROMENCY (617) 227-740
TELEPROME: (617) 227-740
TELEPROME: (617) 227-740
INFORMATION FOR SED ID NO: 1: SEQUENCE CHARACTERISTICS:
LEGISTH: 525 Dase pairs
TYPE: nucled acid
STRANDEDINESS: single
STRANDEDINESS: single
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | FEATURE:
| NAME/KEY: CDS
| LOCATION: 1..525
| FEATURE:
| NAME/KEY: mat_peptide
| LOCATION: 79..525
| US-08-466-793-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.7
Best Local Similarity 59.2
Matches 141; Conservative
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US-08-491-861A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AGCCACGITCACCITCAIGAGGAGGAICGGIGCAICCAGAAGAAAAICCIGAIGCGGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGGAGGCCCAGGAAGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 28.7%; Score 70.4; DB 2; Length 525; Best Local Similarity 59.2%; Pred. No. 7.9e-11; Matches 141; Conservative 0; Mismatches 91; Indels
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: LNI-026CP (IPC-048CP)
TELECOMMUNICATION INFORMATION.
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR END ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STATE: Signification of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Morgenstern, Jay P.
APPLICANT: Morgenstern, Jay P.
APPLICANT: Maleczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Applies from Dog
TITLE OF INVENTION: Deptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: GO State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDLIN TYPE: Floppy disk
COMPUTER: IBN PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: ASCII-text
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/466,793
FILIND DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08466793
Patent No. 5891716
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide 79..525
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY; linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1..525
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 60 Starts: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEX;
; LOCATION;
US-08-467-603-1
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US-08-466-793-1
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                         96 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGGTCGTAAAGGACTTT 147
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1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTT 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 147;
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Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CONKIIN, DAITELL C.
TITLE OF INVENTOR: 11POCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: 159/09/130,663A
CURRENT APPLICATION NUMBER: 60/054,867
RAKLIER PILLING DATE: 1998-06
RAKLIER PILLING DATE: 1997-08-06
SOFTHARE: FASISED for Windows Version 3.0
SOFTHARE: PASISED for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION

APPLICANT: CORLIA, DATE-1 C.

TITLE OF INVENTION: LIPOCALIN HOWOLOG

FILE REPERENCE: 97-24

CURRENT APPLICATION NUMBER: US/09/432,335

CURRENT FILING DATE: 1999-11-02

RARLIER PELLING DATE: 1999-808-06

EARLIER FILING DATE: 1998-08-06

EARLIER FILING DATE: 1997-08-06

FARLIER FILING DATE: 1997-08-06

SOFTWARE: FASSON FOR MAGNETION NUMBER: 60/1054,867

EARLIER FILING DATE: 1997-08-06

SOFTWARE: FASSON FOR MAGNETION NUMBER: 60/1054,867

SOFTWARE: FASSON FOR MAGNETION NUMBER: 60/1054,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: N-terminal Flag linker US-09-130-663-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: NEE-tagged linker US-09-432-335-16
                                                                                                                 RESULT 11
2-09-130-130-663-24
: Sequence 24, Application US/09130663A
: Patent No. 6020163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09432335
Patent No. 6143720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-432-335-16
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US-09-432-335-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouerr March 28.7%; Score 70.4; DB 2; Length 525; Best Local Similarity 59.2%; Preck No. 79e-11; 79e-11; Marches 141; Conservative 0; Mismatches 91; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 AGCCAAGATCACCATGCTGACAAATGGTCAGTGCCAGAACATCACGGTGGTCCTGCACAA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
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     GENERAL TREORATION:
APPLICANT: CORLIA, Darrell C.
TITLE OF INVENTION: LIPOCALIN HONOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US,09/130,663A
CURRENT FILING DATE: 1998-08-05
BARLIER APPLICATION NUMBER: 60/054,867
BARLIER APPLICATION NUMBER: 60/054,867
NUMBER: OF SEQ ID NOS: 30
SOFTWARE: FEASURE OF WINDOWS VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: NEE-tagged linker US-09-130-663-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09130663A, Patent No. 6020163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: mat_peptide
; LOCATION: 79.525
US-08-491-861A-1
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..525
                                                                                                                                                                                                                                                                                                                                                                                          linear
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96 GGATAITCACAGGGACCTGGTACGTGAAGGCCATGGTGGTGGTCGATAAGGACTTT 147
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                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: N-terminal Flag linker US-09-614-022-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 9, 2003, 22:05:05 Job time: 21.8084 secs
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 60/054,867
PRIOR PLING DATE: 1997-08-06
WUMBER OF SEQ ID NOS: 30
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                             SEQ ID NO 24
LENGTH: 147
                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
21.2%; Score 55; DB 3; Length 147;
Best Local Similarity 100.0%; Pred, No. 6.8e-06;
Matches 52; Conservative 0; Mismatches 0; Indels
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                                                                     FILE REFERENCE: 97.24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER PILING DATE: 1999-08-06.6
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER PILING DATE: 1997-08-06
SOVEWARE: FALSED NOS: 30
SOVEWARE: PASCED for Windows Version 3.0
STO ID NO 24
TENCHEL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REPERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/614,022
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,63
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 60/054,867
PRIOR FILING DATE: 1997-08-06
SOFWHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION; N-terminal Flag linker US-09-432-335-24
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FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/614,022
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,663
                       APPLICANT: CONKLIN, DAITELL C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09614022
Patent No. 6365716
GENERAL INFORMATION:
APPLICANT: CORLIA, DATTELL C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: NEE-tagged linker US-09-614-022-16
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Patent No. 6365716
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA.
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
     GENERAL INFORMATION:
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US-09-614-022-16
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US-09-614-022-24
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us-09-099-823-2.rnpb

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Sequence 3730, Ap Sequence 7960, Ap Sequence 217, Appl Sequence 217, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 194, Appl Sequence 2189, Appl Sequence 2189, Appl Sequence 2189, Appl Sequence 10761, Appl Sequence 110761, Appl Sequence 1204, Appl Sequence 199, Appl Appl Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "OS/08099823

"JIGNNT: BILLING-MEDEL, PATRICIA
APPLICANT: COLETYS, TRACEY I.
APPLICANT: COLETYS, TRACEY I.
APPLICANT: RAILAN, PAULA N.
APPLICANT: RANCHEND N.
APPLICANT: RANCHELL, ON D.
APPLICANT: RANCHELL, ON D.
APPLICANT: REACCHIL, ON D.
APPLICANT: REACCHIL, ON D.
APPLICANT: REACCHIL, ON D.
APPLICANT: REACCHIL, ON D.
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: TROUBE, STEPHEN D.
APPLICANT: TROUBE, STEPHEN D.
APPLICANT: TO, BONG
APPLICANT: TO BONG
A
1 10 US-09-878-574-3730

1 10 US-09-813-929-98

2 10 US-09-813-958-217

3 US-09-913-812-31

4 US-09-913-817-31

9 US-09-364-847-20

9 US-09-364-847-34

9 US-09-364-847-34

9 US-09-364-847-34

9 US-09-364-847-34

10 US-09-86-86-1

10 US-09-764-878-377

10 US-09-764-878-377

11 US-09-764-878-377

12 US-09-764-878-377

13 US-09-764-878-377

14 US-09-766-52-824

15 US-09-764-878-377

16 US-09-764-878-377

17 US-09-764-878-377

18 US-09-766-762-281

10 US-09-867-550-1671

10 US-09-867-550-1671
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COMPUTER FRABABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSOR Windows Version 2.0
SOFTWARE: FASTSOR for Windows Version 2.0
SOFTWARE: FASTSOR OF WINDOWS VERSION 2.0
SOFTWARE: FASTSOR OF WINDOWS VERSION 2.0
SOFTWARE: FASTSOR OF WINDOWS VERSION 2.0
FILING DATE: 0.00 JUN-1997
ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
              0000000
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Sequence 1, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 1147, Ap
Sequence 117, Ap
Sequence 1, Appli
Sequence 11878, A
Sequence 11878, A
Sequence 1, Appli
                                                                                                                                                                                                                         (without alignments)
6148.496 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                      February 9, 2003, 21:14:50 ; Search time 18.8877 Seconds
                                                                                                                                                                                                                                                                                                US-09-099-823-2
245
I GGATATCACAGGGACCTGGT......CATGTACCTGCAGGAGCTGC 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_NA:*

11. /cgn2_6/ptodata//puppna/Pcr_NBW_PUB.seq:*
22. /cgn2_6/ptodata//puppna/Pcr_NBW_PUB.seq:*
33. /cgn2_6/ptodata//pubpna/US06_NBW_PUB.seq:*
47. /cgn2_6/ptodata//pubpna/US06_PUBCOMB.seq:*
57. /cgn2_6/ptodata//pubpna/US07_NBW_PUB.seq:*
67. /cgn2_6/ptodata//pubpna/US07_NBW_PUB.seq:*
77. /cgn2_6/ptodata//pubpna/US08_NBW_PUB.seq:*
87. /cgn2_6/ptodata//pubpna/US08_NBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US08_NBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US09_WBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US09_WBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US01_WBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US10_NBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US10_NBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US10_UBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US10_UBW_PUB.seq:*
97. /cgn2_6/ptodata//pubpna/US60_WBW_PUB.seq:*
                                             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-099-823-2
US-09-091-845-1
US-09-099-823-4
US-09-0823-381-1747
US-09-099-823-1
US-09-099-823-1
US-09-099-823-1
US-09-099-823-1
US-09-878-574-11281
US-09-878-574-11281
US-09-878-574-11281
US-09-878-574-11281
US-10-166-359-1
US-10-166-359-1
US-10-166-357-1
US-10-166-372-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408267 seqs, 237001491 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match 1
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Perfect score:
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121 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                            Gaps
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APPLICANT: GRANDOS, EDWARD N.
APPLICANT: KLASS, MICHAEL N.
APPLICANT: KLASS, MICHAEL N.
APPLICANT: KRAYCCHVIL, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: SUGBETEL, CHRISTI
APPLICANT: STOOPE, STEPHEN D.
APPLICANT: STOOPE, STEPHEN D.
APPLICANT: TUT, HOW
TITLE OF INVENTION: POR DETECTING DISEASES OF THE BREAST NUMBER OF SEQUENCES: 27
CORRESPONDENCES: 27

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 6120.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BILLING-MEDEL, PATRICIA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UNN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-099-823-4
US-09-099-823-4
Sequence 4, Application US/09099823
Patent No. US20020018990A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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316 GCTGC 320
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Patent No. USZ0020098497a1
Patent Patent Holloway, James L.
Patent Represention: 0.ee of Human Phermone Polypeptides
Patent Representies Patent Representies
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.Pl
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHRARAFERSTICS.
IEMUTH: 245 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8)...(517)
US-09-951-845-1
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US-09-951-845-1
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Sequence 1747, Application US/09833381

Fatent No. US20020132090A1

Fatent No. US20020132090A1

FAPILICARN: Robleson, Keith E.

TILE REFERENCE: 5800-119

CORRENT PELLING DATE: 2001-04-11

FRICE APPLICATION NUMBER: 09/516,448

FRICE APPLICATION NUMBER: 09/516,448

FRICE REFERENCE: 5000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 1747

LENGTH: 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ACAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGG 119
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                                                                                                                                                                                                                                                                                                                61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                 121 AGCCACGIICCACGIICCAIGAGGGAGGAICGGIGCAICCAGAAGAAAAICCIGAIGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGATATCACAGGGACCTGGTA-CGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGG 59
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Live 0; Mismatches 0; Indels
                                                                                                               Length 692;
                                                                                                                  Query Match 100.0%; Score 245; DB 10; Best Local Similarity 100.0%; Pred. No. 1.1e-60; Matches 245; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 AAGACGGAGGAGCCTGGCAAATACAGCGC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.0
Matches 207; Conservative
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-099-823-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1747
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US-09-833-381-803/c
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US-09-833-381-1747
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                                                                                                                                                             121 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                               181 GACGGAGGAGCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
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GUEN, MAURICE

APPLICANT: COLETYS, TRACET L.

APPLICANT: FRIEDAN, PAULA N.

APPLICANT: GRANADOS EDWARD N.

APPLICANT: GRANADOS EDWARD N.

APPLICANT: GRANADOS EDWARD N.

APPLICANT: GRANADOS EDWARD N.

APPLICANT: GRESELL, CHRISTI

APPLICANT: STRUCHYLL, JOHN C.

APPLICANT: STRESELL, CHRISTI

APPLICANT: STREST: 100 ABDOCT PADPRESS:

CORRESPONDERS ADDOCT LABOCATOLISS

STATE: 100 ABDOCT PAIK ROAD

CITY: ABDOCT PAIK

CITY: ABDOCT PAIK

CONPETER READABLF

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TEM Compatible
COMPARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823
FILING DATE:
CLASSIFCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UUN-1997
ATTORNEY/ARENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
RESTERNEY/OCKET WINBER: 6120.US.P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 847/938-2623
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5

Gaps

5;

Gaps

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Length 236;

us-09-099-823-2.rnpb

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113 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Morgenstern, Jay P.
APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzey
APPLICANT: Braindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allegenic Proteins and Peptides from Dog TITLE OF INVENTION: Dander and Uses Therefor NUMBER OF SEQUENCES: 104
CORRESPONDENCE JOHNESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: Set State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.6%; Score 124; DB 10; Length 23 Best Local Similarity 100.0%; Pred. No. 1.9e-26; Matches 124; Conservative 0; Mismatches 0; Indels.
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NAME: MANDRAPION:
NAME: MANDRAPION:
REGISTRATION NUMBER: 36,207
TERESCOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                               6120.US.P1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,671
PILIN DATE:
  APPLICATION NUMBER: 08/679,354
PILIME DATE: 20-JUN-1197
ATTORNEY AGENT INFORMATION:
NAME: BECKET INFORMATION:
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEPHONE: 847/938-1623
TELER:
INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NG-DOS
SOFTWARE: ASCII-text
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APPLICATION NUMBER: 08/491,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-374-671-1
Sequence 1, Application US/09374671
; Patent No. UG20020012963A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGHH: 236 base pairs
TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOGY: linear
US-09-099-823-1
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TELEFAX: (617) 742-4214
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ZIP: 02109
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Sequence 803, Application US/09833381

Factor No. US2020132909A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: No. US2020132090Alel Nucleic Acid and Protein Homologs.
TITLE OF INVERTION NUMBER: 1800-113

FILE REPERBACE: 8800-113

FRICH REPERBACE: 8800-113

CURRENT FILING DATE: 2000-04-11

PRIOR PRILIKG DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 205-29

NUMBER OF SEQ ID NOS: 205-20

SEQ ID NOS: 205-20

SEQ ID NOS 803

LENGTH: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GTGTCCCCAGTGAAGGTGACACCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 ATGAGGGAGGATCGGTGCATCCAGAAAATCCTGATGCGGAAGACGGAGGAGCTGGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.5%; Score 150.6; DB 10; Length 501; Best Local Similarity 97.0%; Pred. No. 6.4e-34; Matches 164; Conservative 0; Mismatches 4; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COHEN, MAURICE
APPLICANT: COLETTS, TRACET L.
APPLICANT: COLETTS, TRACET L.
APPLICANT: GORDON, JULIAN N.
APPLICANT: GRANDOOS, EDWARD N.
APPLICANT: GRANDOOS, EDWARD N.
APPLICANT: HONGES, MICHAEL R.
APPLICANT: KRANCCHVIL, JON D.
APPLICANT: KRANCHVIL, JON D.
APPLICANT: KRANCHVIL, JON C.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: FOR DETECTING DISEASES OF THE BREAST NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 AAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 AAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGC 245
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park Road
CITY: Abbott Park
STATE: 11
COUNTRY: USA
ZIF: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09099823
Patent No. US20020018990al
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-099-823-1
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Sequence 11878, Application US/09878574
; Sequence 11878, Application US/09878574
; Retent No. US200201105881
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Thomson, Michael D.
; TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TILLE OF INVENTION: Plants
FILE OF INVENTION: Plants
CURRENT FILING DATE: 2001.12-21
PRIOR PILING DATE: 2001.12-21
PRIOR FILING DATE: 1099-06-14
; SED IN 01 1878
; ENGREN: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Byrun, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Trompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REPRENEUR: 38-21(15401)8
CURRENT APPLICANION NUMBER: 08/09/874
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER: OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GGAGGACAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 GTTGGAAGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 GCCGAAGGGCCAGAAGAAGATCTCGAAGGAAGAAGAGGAGCGAGAAGAAGAAGAAGAAGAAGCAC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 GGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38.2; DB 10; Length 299;
Pred. No. 0.046;
0; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-056-01-B1-D8
US-09-878-574-59
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA CANTEM: Glycine max OTHER INFORMATION: CLOBE ID: 701065017H1 US-09-878-574-11878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/09878574 Patent No. US20020110548A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.6%;
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Best Local Similarity 50.8
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.6
Best Local Similarity 50.8
Matches 91; Conservative
                                                                 RESULT 10
US-09-878-574-11878
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US-09-878-574-59
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LENGTH: 385
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Sequence 11281, Application US/09878574

Patent No. US20020110548A1

SEREMAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael J.

TITLE OF INVERTION: Plants

FILE REFRENCE: 38-21(15401)8

FILE REFRENCE: 38-21(15401)8

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/33,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 11281
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                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0.045;
0; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                                      Score 70.4; DB 10; Length 525; pred. No. 3.8e-11; 0; Mismatches 91; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANIEM: Glycine max
; CTHER INFORMATION: CLONE ID: 701064263H1
US-09-878-574-11281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%;
50.8%;
                                                                                                                                                                                                                                                                                                           Query Match 28.7%;
Best Local Similarity 59.2%;
Matches 141; Conservative
                                                 LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.6
Best Local Similarity 50.8
Matches 91; Conservative
               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 mat_peptide
79..525
                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                        1..525
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US-09-878-574-11281
                                                                                                                                                                                                            FEATURE:

NAME/KEY:

LOCATION:

US-09-374-671-1
                                                                                                                                                                           NAME/KEY:
LOCATION:
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING THE INTERACTION TITLE OF INVENTION: BETWEEN THE APJ RECEPTOR AND THE HIV VIRUS
                                                                                                                                                                                                                                                                                                                                                                                               148 TCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gabs
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                                                                                                                                                                                                        Query Match
14.78; Score 36; DB 9; Length 1464;
Best Local Similarity 54.58; Pacd No. 0.29;
Matches 72; Conservative 0; Mismatches 60; Indels
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CURRENT APPLICATION NUMBER: US/10/166,113
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 09/149,045
PRIOR FILING DATE: 1998-09-08
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US-10-166-113-1/C
Sequence 1, Application US/10166113
Publication No. US20030008279A1
SERMEAL INFORMATION:
APPLICANT: DAMS, ROBERT W
APPLICANT: HESELEGESER, JOSEPH E.
APPLICANT: HESELEGESER, JOSEPH E.
APPLICANT: HORIK, RICHARD
APPLICANT: MITROYL, BRANISLAVA
NUBLICANT: ZHOU, YIQING
NUBLICANT: ZHOU, YIQING
NUBLICANT: APPLICANT: APP
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; Publication No. US20030008376A1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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; LOCATION: (199)..(1338)
US-10-166-113-1
                                                                     ) NAME/KET: CDS
; LOCATION: (199)..(1338)
US-10-166-359-1
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ORGANISM: Homo sapiens
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453 CCACAGGGGCAG 442
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US-10-166-357-1/c
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: In Thomson, Michael D.
APPLICANT: In Thomson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: UNCLEIC Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: UNCLEIC Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: UNCLEIC Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION UNUBER: US/09/878,574
CURRENT APPLICATION UNUBER: US/09/873,535
PRIOR APPLICATION UNUBER: 1999-06-14
SEQ ID NOS: 15775
SEQ ID NOS: 15775
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING THE INTERACTION
TITLE OF INVENTION: BETWEEN THE ADJ RECEPTOR AND THE HIV VIRUS
                            115 GIIGGAAGCCACGIICACCIICAIGAGGGAGGAICGGIGCAICCAGAAGAAAAICCIGAI 174
                                                                     115 GTTGGAAGCCACGTTCACCTTCATGAGGAGGATCGGTGCATCCAGAAGAAAATCCTGAT 174
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                                                                                                                                                                   175 GCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACC 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Glycine max
; OTHER INFORMATION: CLone ID: LIB3028-026-Q1-B1-G3
C9-9878-574-2305
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CURRENT APPLICATION NUMBER: US/10/166,359
                                                                                                                                                                                                                                                                                                                                                                           US-09-878-574-2305; Septication US/09878574; Sequence 2305, Application US/09878574; Patent No. US20020110548A1; SENERAL INFORMATION:
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PRIOR PRIZING NUMBER: 09/149,045
PRIOR FILING DATE: 1998-09-08
NUMBER OF SEQ ID NOS: 8
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APPLICANT: FAULDS, DARYL
APPLICANT: HESSELGESSER, JOSEPH E.
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APPLICANT: MITROVIC, BRANISLAVA
APPLICANT: ZHOU, YIQING
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LENGTH: 1464
TYPE: DNA
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37.6 431 9 AA936288 AA936288 AA936288 AA936288 AA936288 AA936288 AA936288 AA936288 AA936288 AA936289 AA936285 BBG18259 BA618259 BA618259 BA618259 BA618269 AA60385 AA460385 AA460385 AA460385 AA460385 AA936286 BA60389 BA60389 BA60389 BA60389 BA603580 BA603580 BA603580 BA603590 BA603590 BA603590 BA603590 BA603559 BA603559 BA603559 BA603550 BA603550	17 43.8 17.9 224 10 AN316476 A	4.18 17.1 647 13 B1954686 4.18 17.1 663 13 B1957662 4.18 17.1 805 12 B726509 4.18 17.1 875 12 B7267309 4.18 17.1 875 12 B7267309 4.1.4 16.9 500 10 B1421286 40.4 16.5 620 10 B1442286 40.4 16.5 621 14 B060557 40.6 16.3 581 9 AL588422 40 16.3 581 9 AL588428 40 16.3 581 9 AL588428 40 16.3 601 12 B709987 39.8 16.2 442 12 B7898928	443 12 BGB13980 618 13 BJ045011 606 13 B1479760 ALIGNMENTS	RESULT 1 AW313637, AW513637 532 bp mRNA linear EST 03-MAR-2000 LOCUG LOC	REFERENCE (bases It to 532) AUTHORS AUTHORS NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), TITLE Tunco Gene Index JOHENEL ORDHALISTER CALL STRAUSBERG, Ph.D. COMMENT CONTACT: Robert Strausberg, Ph.D. Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmart-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CLOne distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at: Image.linl.gov/lmage/html/iresources.shtml
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: February 9, 2003, 22:05:30 ; Search time 681.035 Seconds (without alignments)	TACCTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	um DB seq length: 0 um DB seq length: 0 processing: Minimum Match 0%		15: em_estfun:* 16: em_estfun:* 17: 9b_gss:* 17: 9b_gss:* 18: em_gss. bun:* 19: em_gss. lun:* 20: em_gss. lun:* 21: em_gss. lun:* 22: em_gss. lun:* 23: em_gss. lun:* 24: em_gss. lun:* 25: em_gss. lun:* 26: em_gss. lun:* 27: em_gss. lun:* 26: em_gss. lun:* 27: em_gss. lun:* 26: em_gss. lun:* 27: em_gss. lun:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result No. Score Match Length BB ID C 1 168 68.6 532 10 AW513637 AW513637 Xo47h10.x C 2 145 59.2 499 9 A121910 AA213617 G106103.x C 3 134.8 55.0 513 9 AA377608 BP193883 245614 MA C 5 128.8 52.6 477 9 A152147 AA251747 G490612.x 6 97.8 39.9 494 14 R47029 R47029 Y358 Rat in

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RESULT 3
AA977608/c
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Induction of 1997)

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Email: cgapbs r@mail.nih.gov

This close is available royalty-free through LINL; contact the Induction of Induction of Induction of Experimental of Experiments of
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                                                                                                                                                                                                                                                                                                                                              /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"
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Best Local Similarity 92.2%; Pred. No. 4.2e-32;
Matches 177; Conservative 0; Mismatches 15; Indels 0; Gaps
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                                                                                                                                                   /organism="Homo sapiens"
/db_xref=-taxon:1960e"
/clone=_TRAGE:2707171"
/clone=_lib="Ncl_CGAP_Ut1"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH108"
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Possible reversed clone: polyT not found Seq priner: -400P from Gibco High quality sequence stop: 316.
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Particle anothic of plasmid DNA from three normalized libraries (facil long plant), state in 15 state; see Fil panis amounts of plasmid DNA from three normalized libraries (facil long plant), state in 15 state; see Fil panish anothic of plasmid DNA from three normalized libraries (facil long plant), state in 15 states as circles were made in vitro. Pollodiang HPP publication reaction. The sum as tracer in a subtractive physiciation reaction. The sum as tracer in a subtractive physiciation reaction. The sum as tracer in a subtractive physiciation reaction. The sum as tracer in a subtractive physiciation reaction. The sum as tracer in a subtractive physiciation contact of 5,000 clones made from the same 3 inbracte. The pols occases and Mr Patina Bonaldo. 2 others

Scoone 15 siniarity 93.0%; bread No. 24-25; bast Local Siniarity Siniarit
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Gaps

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BASE COUNT ORIGIN

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/documber_univor_univor_

/documber_organ: pooled; Vector: pTyT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from thee normalized libraries (fetal lung NbHL30W, testis NHT, and B-Cell libraries (fetal lung NbHL30W, testis NHT, and B-Cell NCI_CGAP_GCB1) were mixed, and ss circles were made in virco. Pollowing Har purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302097, 682632-687239, 726408-7782711, and 722096-713399. Subtraction by Bento Soares and M. Patina Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A1551747

qh90f12.x1 Scares_NFL_T_GBC_51 Homo sapiens CDNA clone
INAGE:1854287 3' similar to TR:Q63613 Q63613 ODORANT-BINDING
PROFEIN. ', mRNA sequence.
A1251747.1 G1:3848276
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4/17)
NOI-CGAP http://www.nobi.nlm.nlh.gov/noicgap.
NOI-CGAP intp://www.nobi.nlm.nlh.gov/noicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAS Consortium (info@lmage.llnl.gov) for further information.
Seg primer: 40UP from Gibco
High quality sequence stop: 396.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 AGTIGGAAGCCACGITCACCITCATGAGGGAGGAICGGIGCAICCAGAAGAAAAATCCIGA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                      121 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 180
                                                                                                                                                                                                                                                                                                  1 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 60
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Pred. No. 9.9e-24;
0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    294 AACCGGGGAGCTGCCGAATACAGCTCCAATGCCGGCAAGAAGC 337
                                                                                                                                                                                                                                                                                                                                                                          181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, 477
/organism="Homo sapiens"
/db_xref="texon:9606"
/dlose="InAGE:184289"
/clone=lib="Soares_NBF_T_GBC_SI"
/lab_host="DH10B"
  Best Local Similarity 75.0%;
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Fars: 402 7762 4396

Fars: 402 7762 4390

Fars: 402 7764 4390

Fars: 402 7764 4390

For Single pass sequencing. Bases called and alt_trimmed with phred and -minatch 12 options.

POR PRIMETS
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1 (bases 1 to 337)

Smith.T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.E., Heaton, M.P., Laegreld, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertes, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
        726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 133 c 158 g 134 t.
                                                                                                                                                                                                                                                                77 GIGICCCCAGIGAAGGIGACAGCCCIGGGCGGIGGGAAGIIGGAAGCCACGIICACCIIC 136
                                                                                                                                                                                                                                                                                                                                     137 A-TGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGG 195
                                                                                                                                                                                           Gaps
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                                                                                                                                       DB 9; Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                       196 CARATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 134.8; DB 9; Length 5
Pred. No. 8.8e-24;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenal, and endometrium."
110 c 110 q 45 t
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/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORMARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 76 row: C column: 21
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="MARC 2BOV"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF193883.1 GI:11077252
                                                                                                                                    Query Match
Best Local Similarity 94.7%;
Matches 161; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
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DEFINITION

RESULT 4

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ORGANISM

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SOURCE

VERSION

REFERENCE AUTHORS

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Query Match BASE COUNT ORIGIN

FEATURES

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/documber_burbor.
//documber_burbor.
//documber_bur
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (basea 1 to 431)
NOI-GAP http://www.nobi.nlm.nih.gov/noicgap.
NOI-GAP Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 344.
Location/Qualifiers
1..431
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                                                                        181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                                                                                               37.6%; Score 92.2; DB 9; Length 431;
96.9%; Pred. No. 4e-13;
Live 0; Mismatches 3; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 bp mRNA linear EST 29-Mi on75fil.si Scares NFL_T.GBC_S1 Homo sapiens cDNA clone IMAGE:1562541 3' similar to TR:Q63613 Q63613 ODORANT-BINDING PASSGERS , mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:1562541"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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AA936288.1 GI:3094206
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Unpublished (1997)
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Best Local Similarity 96.9
Matches 94; Conservative
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                                                                                                                                                                                                                                   241 GCTGC 245
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AA936288/c
LOCUS
DEFINITION
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AI877465
LOCUS
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//ab.ost="Xi-] blue"
//ab.ost="Xi-] blue"
//ab.ost="Yi-] blue"
//ab.ost="Yi-] blue"
//ab.ost="Yi-] bluescript II SK -; Site_1: Eco RI; Site_2:
//ab.ost="Yi-] bluescript II SK -; Site_1: Eco RI; Site_2:
//ab.ost="Yi-] bluescript II SK -; Site_1: Eco RI; Site_3:
//ab.ost="Yi-] bluescript Incisors from 3-4 week old rats
//ab.ost="Yi-] was constructed in the IZAP
//ab.ost="Yi-] rate on the IZAP
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//ab.ost="Yi-] rate of Site of Site on the IZAP
//ab.ost="Yi-] rate of Site of Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              R47029 494 bp mRNA linear EST 15-MAY-1995 X358 Rat incisor (noncalcified tissues) Rattus norvegicus cDNA clone Y358 5' end similar to odorant-binding protein (RYZG12), mRNA
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Matsuki,Y., Makashima,M., Amizuka,N., Warshawsky,H., Goltzman,D.,
Yamada,Y. and Famada,Y.
A compilation of partial sequences of randomly selected cDNA clones
from the rat incisor
J. Dent. Res. 74, 307-312 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Developmental Biology, National Institute of Dental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 GAAGAGACCTATGAAAGTGTTCCCTATGACTGTGACAGCCCTGGAAGGAGGGGGACTTAGA 208
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                                               0; Gaps
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Live 0; Mismatches 92; Indels 0;
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Building 30, Room 405, Bethesda, MD 20892
Tel: 301496211
Fax: 3014020897
Email: yamada@yoda.nidr.nih.gov
Seg primer: AACAAAGCTGGAGCTCCACC.
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//Organism="Rattus norvegicus"
/strain="Sprague-Dowley"
/db_xref="taxon:10116"
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Rattus norvegicus
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                                                                                                                                                                                                                                                        356 TGCAGGAGCTGC 345
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Contact: Yoshihide Hayashizaki
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Roisenter (GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
Tel. Sinstitute of Physical and Chemical Research (RIKEN)

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Tel. S1-45-503-9215
Fax: S1-45-503-9216
Fax: Mornalization and subtraction of cap-trapper-selected connact operate full-length cDwa libraries for rapid discovery of new prepare full-length cDwa libraries for rapid discovery of new prepare full-length cDwa libraries for rapid discovery of new prepare full-length cDwa libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
Fax: Rawal, Y., Yoneda, Y., Ishkawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Rawal, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Rawal, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, T. Farwal, Henraried Sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
10 (11), 1757-1771 (2000)
10 (11), 1757-1771 (2000)
11 (11), 1757-1771 (2000)
12. and Hayashiarki, Y. Shibata, K., Itoh, M., Carninci, P., Sugahara Y. and Hayashiarki, Y. Computer-based methods for the mouse full-length cDNA encylopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) sonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) (2004). Shibagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa Hayashizaki, Y. Ribada, K. and
                                                                                                                                                                                                                                          Arakawa, T. Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Bara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komno, H., Kouda, H., Koya, S., Matsuyama, T., Miyazaki, A., Nomira, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Saruki, H., Muramatsu, M., and Hayashizaki, Y. Takeda, Y., Tanaka, Y., Tayawa, A., Shiraki, T., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone="5430417003"
/clone_lib="RIKEN full-length enriched, 6 days neonate
nusculus cDNA clone 5430417003 5', mRNA sequence.
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Location/Qualifiers
                                BB618259
BB618259.1 GI:16457878
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Oppublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
         udiod09.rl Scares NWPu Mus musculus cDNA clone IMAGE:1434737 5' similar to TR:Q63613 Q63613 ODCRANT-BINDING PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector to vector length is Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 503.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
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/lab_host="DH10B"
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Dikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Bases Ir 0 626)

2 Arakawa, T., Carnindi, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.

4 Hirando, K., Hori, F., Ishili, Y., Hto, M., Kawai, J., Konno, H., Kouda

M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Shinate, K., Shinate, K., Shinate, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Muramatsu, M., Tagawa, A., Shirati, F., Takada, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y., Takada, Y., Tanaka, T., Tana
transcriptase and subsequently enriched for full-length by captrapper. CDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GARAGARATHTCHATHATHATHATHCCCCCCCCCCCC 3']. CDNA was cloned into the KhoI and BamHI sites. Vector: a modified paluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI.
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BB028765 RIKEN full-length enriched, 6 days neonate head Mus
BB028765 BB028765 GI:16258092
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Contact: Yeshihide Hayshiazaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibeta.Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to prepare full-length cDNa libraries for rapid discovery of new
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61.0%;
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Matches 147; Conservative
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, 6 days neonate
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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ed rat, norvegicus, Bento Soares
15 5' end, mRNA sequence.
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/lab_host="Soln"
/hote="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: %hote="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: %hote="Tainsted insert size approx:1 kb"
153 c 148 g 124 t
                                                                                                                                                                                                                                                                Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Lee,N.H., Glodek,A., and Adams,M.D.
Karlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIG946"
/clone=lib="Rat gene index, normalized rat, norvegicus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 GAAGITIGGAICTGIGICACTCCCAIGAAAATCAAGACCCIGGAAGGGGGCAACCI 212
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The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
The 1301)-838-9529
The (301)-838-9208
Examt: Nhleedetigr.org
This clone is available through the ATCC, contact the ATCC tel#703-365-7700 for further information
Seq primer: MI3 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTAC 232
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500754 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BM087898 GI:16998526
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Rattus norvegicus CDNA clone RGIGT45 5' er
                                                                                                                  594 bp
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64 TCATGTACCTGCAGGAGCTGC 84
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AW920286.1 GI:8086095
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Unpublished (1998)
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REALIGET.L., Allen.M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Hillier.L., Allen.M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997

L. Onpublished (1997)

Contact: Wilson RK
Washington University School of Medicine
4444 Forset park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 134 c 108 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pr713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: 1st strand cDNA bolylinker; Site_1: Not I olite_2: Eco RI: 1st strand cDNA was prepared from mNna Obtained from Clontech Laboratories inc., and primed with a Not I - oligo(dr) primer [5' rgrnacCaarcrGaaGGGGGGGGCGCCCAarrrTrTrTrTrTrTrTrTT 3'].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                           AA460385 415 bp mRNA linear EST 09-JUN-1997 zxlie06.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795778 5' similar to TR:G207551 G207551 ODORANT-BINDING PROTEIN: ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further infoxmation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 AAATCCTGATGCGGAAGACGGAGGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79.4; DB 9; Length 415;
Pred. No. 6.5e-10;
0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GACGGAGGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 240
                                                         Putative full length read
The vector to vector length is
Seq primer: -2mil rev2 Er from Amersham.
Location/Qualifiers
1 . .415
/GDarism="Room saptens"
/GDarief="GIB: 603983"
/GD.xref="Laxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:795778"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 32.4%;
Best Local Similarity 98.8%;
Matches 80; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                      AA460385
AA460385.1 GI:2185598
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BF405590 454 bp mRNA linear EST 28-NOV-2000 UI-R-CA1-bix-g-24-0-UI.sl UI-R-CA1 Rattus norvegicus CDNA clone
                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
%0.98094.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRImers
  /note==vector: pcnv SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longisiams muscle.

1 124 c 152 g 75 t
                                                                                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 GGABABGGTATCTGABGGCCGTGACCACAGACCAGGGCGTTCCCGGG---AAGAATCAGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 GGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 CCTTCATGAGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGAAGGAGGAGC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.3%; Score 57; DB 12; Length 438; 57.9%; Pred. No. 0.00027; tive 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib=WaRG 3BOV"
//issue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 CTGGCAAATACAGCGCCTATGGGGGCAGG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORRARD: AGGAAAGAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 49 row: A column: 5
Seq primer: ATTRAGGTGACACTATAG.
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BF405590.1 GI:11393565
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Matches 121; Conservative
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Rattus norvegicus
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bos.

10 (bases 1 to Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Bolt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                               EST 25-APR-2001
                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /.note-"Vector: pGNV SPORTG; Site_1: Not1; Site_2: SalI; Library made from pooled tissue from testis, thymus, semitemborosus muscle, longissimus muscle, pancreas, actional, and endometrium."

130 c 158 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 GGACGTGTCAGGAAAATGGTATCTGAAGGCCGTGACCACAGACCAGGACGTCCCGGG-- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AGCCACGIICACCIICAIGAGGGAGGAICGGIGCAICCAGAAGAAAAICCIGAIGCGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 GGCCAAAGTCACGTCGCGGGTTGATGGTCAGTGCCAGGAGCAACGAGCCTGGAGCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.1%; Score 61.6; DB 13; Length 462; Best Local Similarity 58.2%; Pred. No. 1.9e-05; Matches 128; Conservative 0; Mismatches 89; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 bp mRNA linear 269132 MARC 3BOV Bos taurus cDNA 5', mRNA sequence. BF603580.1 GI:11701336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 AACCAACGATCCTGGCAGATACACAGCCTACGGGGGCCAAG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGGAGG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 139 row: M column: 4
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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us-09-099-823-2, rst

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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
Program for Rat Gene Discovery and Mapping
Discovery of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
751: 319 335 9565
Email: Inscoareselblue, weeg uiowa.edu
The sequence contained an oilgo-dT track that was present in the
Oligonic ONA and therefore this may represent a bonafide poly A
tail: The sequence tag present in the clNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized testis library cDNA library Preparation: M.B. Soares Iab
Clone distribution: clones will be available through Research
Seq primer: MIS Forward
POLIXA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                  " (bases 1 to 454)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GIGICCCCAGIGAAGGIGACAGCCCIGGGCGGIGGGAAGIIGGAAGCCACGIICACCIIC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 AIGAGGGAGGATCGGTGCATCCAGAAGAAAATCCIGATGCGGAAGACGGAGGAGCCTGGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 CTGATTTCAGGACGGTGCCAGGAGATGAGCACTGTCCTAGAGAAGACAGATGAACCTGGC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.8%; Score 53.4; DB 12; Length 454; Best Local Similarity 59.6%; Pred. No. 0.0022; Matches 90; Conservative 0; Mismatches 61; Indels 0; Gaps
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                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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TAG_SEQ=ACGCAG"
a 98 c 130 g
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Search completed: February 10, 2003, 04:58:07 Job time: 694.035 secs

SUMMARIES

Length DB

Sequence
Homo sapi

Sequence Homo sapi Sequence

Mon Feb 10 11:11:49 2003

Run on:

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

em_htg_mam:* em_htg_vrt:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. RESULT 1 AX454620/c LOCUS February 9, 2003, 22:02:40; search time 1097.85 Seconds
(without alignments)
8933.518 Million cell updates/sec 337 1 GGGGAAAAGGACTTTATTT......TAGTGGTCCCTCCTGGGCAG 337 GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapext 1.0 em_htg_other:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-09-099-823-3 gb_ba:*
gb_htg:*
gb_in:*
gb_om:*
gb_ov:*
gb_pat:*
gb_ph:* gb_ro:*
gb_sts:*
gb_sy:*
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gb_vi:* em_ba:* em_fun:* em_hum:* em_in:*
em_on:*
em_or:*
em_ov:*
em_ov:* GenEmbl:* em_un Perfect score; Scoring table: Database: Sequence:

AV251024 Homo sapi AX204078 Sequence AX451247 Sequence AX204081 Sequence AX204081 Sequence AX204081 Sequence AX251025 Homo sapi AC002208 Genomic s AL732161 Homo sapi AL732161 Homo sapi AL732164 Human DNA AL7321029 Homo sapi AL73161 Homo sapi AL73161 Homo sapi AL73161 Homo sapi AL751029 Homo sapi AL751020 Homo sapi AR76744 Rat odorant EC027556 Mus muscu XAZ14552 Sequence AR76747 H. sapiens m AF070675 Sequence EL1541 Mouse CDNA AN70866 R. Norvegicu XZ3166 R. Norvegicu PAT 06-JUL-2002 S77587 VEG protein AR204091 Sequence AF319463 Macropus Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. AX454620 Sequence AX491098 Sequence DNA AX454620 739 bp I Sequence 205 from Patent WO0208284. ALIGNMENTS MUSVNSPIIB RNVEGP2B RNVEGP RATTY2G12A BC027556 AC016427 BSA251020 AX454620 AX454620.1 GI:21713934 996.4 998.8 998.8 998.8 998.8 998.8 998.8 998.8 998.8 998.8 998.8 999.8 99 Homo sapiens human. 133 131.4 1129.8 1129.8 1129.8 1129.8 1129.8 82.6 82.6 81.4 DEFINITION ORGANISM REFERENCE AUTHORS VERSION KEYWORDS .

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180 511 451

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)
Pitiot, G., Lacazette, E. and Gachon, F.
polypeptides puman proteins fixing hydrophobic ligands;
polypeptides and polynucleorides coding for said polypeptides and
uses thereof
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 Length 739;
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99.5%; Score 335.4; DB 6; Length 99.7%; Pred. No. 1.2e-82; Live 0; Mismatches 1; Indels
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Sequence 13 from Patent WO0112806.
AX083548
AX083548.1 GI:13185358
           Query Match
Best Local Similarity 99.7
Matches 336; Conservative
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                Jacorders involving anglogenessis
Patent: WW 0.020384.A. 205 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Genther, Bansperer (US); Gerritaen, Mary E. (US); Goddard,
Audrey (US); Geodwski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US);
Paoni, Nicholas P. (US); Stephan, Jean-Philippe F. (US);
Ratanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
I. (US)
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Enkaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarihini; Hominidae; Homo.
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Patent: WO 0200690-A 205 03-JAN-2002,
Genetcch, Inc. (US)
Location/Qualifiers
1. 739
/organism="Homo sapiens"
/db.xref="Haxon:9606"
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       and \ensuremath{\text{Me}}.\ensuremath{\text{W}}. Compositions and methods for the diagnosis and treatment of
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Pred. No. 1.2e-82;
0; Mismatches 1; Indels 0;
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Sequence 205 from Patent W00200690.
AX491098 1 G1:22323886
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 207 c 205 g 117
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ISM Homo sapiens

Bidaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Enkaryota; Los (76)

1 (bases 1 to 676)

1 (bases 1 to 676)

RS odorant-binding human proteins fixing hydrophobic ligands:

Odorant-binding human proteins fixing hydrophobic ligands:

Odorant-binding human proteins fixing hydrophobic ligands:

polypeptides and polynuclectides coding for said polypeptides and

uses thereof

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Anote="CANA2098 (676) - forme classique (hOBPIID-alpha)"

//do.xref="Laxon:9606"

//do.xref="GANA2098 (676) - forme classique (hOBPIID-alpha)"

//do.xref="GANA2098 (676) - forme classique (hOBPIID-alpha)"
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                                       133 CCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAAATGTCCTCCTCCAAGA 192
                                                              Query Match 96.4%; Score 325; DB 6; I Best Local Similarity 100.0%; Pred. No. 9.4e-80; Matches 325; Conservative 0; Mismatches 0;
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Sequence 9 from Patent W00112806.
AX08354 AX083544.1 GI:13185354
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/codon_start=1
/codon_start=1
/product="pure light of odorant binding protein bg"
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/db_xref="GI:6900081"
/db_xref="GI:6900081"
/cranslation="MKILEIGHULIGHAALSFTLEEEDEGGSVHPEENPDAEDGGAWQ
/cranslation="MKILEIGHULIGHAALSFTLEEEDEGGSVHPEENPDAEDGGAWQ
/rganshathpacaAggsGFPHILLIGRAPWGPAPHGRACG"
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2 (bases 1 to 542)

Direct Submission

Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clemont Ferrand cedex01 63001, FRANCE

Location/Qualifiers

J. 542

/ Organism="Homo sapiens"
// Chromosome="9"
// Map="9434"
                                                                                                                                                                                                                                                                                                                                                                                                                         HSAZ51028 542 bp mRNA linear PRI 02-FEB-2000
Homo, sapiens mRNA for putative odorant binding protein bg (OBFIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 542)
A novel human obstant A.M. and Pitiot, G. and prior, G. anovel human obstant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and genital spheres

Hum. Mol. Genet. 9 (2), 289-301 (2000)
20076326
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       253 TCCTACCCACAAGCITTCCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAA 312
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ilarity 100.0%; Pred. No. 9.3e-80;
Conservative 0; Mismatches 0; Indels
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AJ251028
AJ251028.1 GI:6900080
OBFLID gene; odorant binding protein.
Homo saplens.
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Indels

Length 676;

PAT 28-FEB-2001

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1 (bases 1 to 782)
Pitiot, G., Lacazette, B. and Gachon, F. Odorant-binding human proteins fixing hydrophobic ligands: polypeptides may polynucleotides coding for said polypeptides and uses thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patent: WO 0112806-A 11 22-FEB-2001;
Daiversite d'Auvergne (FR): Pitiot, Gilles (FR)
Cocatioh/Qualifiers
1.782
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Gachon A.M.
Gachon A.M.
Submitsed (26-007-1999) Laboratoire de Biochimie Medicale - INSERM 9384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location Per and Codex01 63001, FRANCE
Location Ferrand Codex01 63001, FRANCE
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Incazette. B., Gachon. A.M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from genemate duplicons at 9434; differential expression in the oral and genital spheres
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               253 TCCTACCCACAAGCTTTCCCATGTGGAGCACCCCCATGGTGCTGGTGTTTGCAGTAAA 312
                                    0; Gaps
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100.0%; Pred. No. 9.4e-80;
Live 0; Mismatches 0;
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AJ551026.
AJ551026.1 GI:6900076
OBPID gene; odorant binding protein.
Homo sapiens.
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Eukaryota, Metazoa, Chordatas; Catarrhini; Hominidae; Homo.
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia: Lo 676;
Pitiot, G., Lacacette, B. and Gachon, F.
Pitiot, G., Lacacette, B. and Gachon, F.
Odorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polypucleorides coding for said polypeptides and uses thereof
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patent: WO 0112806-A 1 22-FEB-2001;
patent: WO 0112806-A 1 22-FEB-2001;
Universite d'Auvergne (FR) ; Pitiot, Gilles (FR)
Location/Qualifiers
1 . 676
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                          482 AGAIGIAGIGGICCCTCCTGGGCAG 458
313 AGAIGIAGIGGICCCICCIGGGCAG 337
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TPALWEALAIDTIRKLRIGTRRPRIRMGGEAHVPAGAAQEGPLHILLQRPAPWGPAPH
                                                                                                                       HSAZ51027 782 bp mRNA linear PRI 02-FEB-2000 Homo sapiens mRNA for putative odorant binding protein bb (OBFIIb
                                                                                                                                                                                                                                                                                                                           Eukaryoza, metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryoza, Eukeria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 782)
Lacazette, Gachon, A.M. and Pitiot, G. A. Dander, Manna A. Dovel human odcrant-binding protein gene family resulting from genomic duplicons at 9934; differential expression in the oral and
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Direct Submission
Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM
Submitted (26-OCT-1999) Laboratoire de Medecine, 28, place Henri
U384, Universite d'Auvergne - Faculte de Médecine, 28, place Henri
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1. 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="OBPIID"
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Best Local Similarity 100.0%; Pred. No. 9.5e-80;
Matches 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              genital spheres
Hum. Mol. Genet. 9 (2), 289-301 (2000)
20076226
10607840
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OBFILD gene; odorant binding protein.
Homo sapiens.
Homo sapiens
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43. .540
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Gachon, A.M.
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                                                                                                                                                                   DEFINITION
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PAT 28-FEB-2001

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/organism="Homo sapiens"
/db_xref="taxon:9606"
43. 483
/note="cDN3396 (725) /SM12 (hOBPIIa-beta)"
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RELPGTDDYYFTCKDQRAGGLRYMGSLVGPCRCPHVGSPGHLFCR"
ELLPGTDDYYFTCKDQRAGGLRYMGSLVGPCRCPHVGSPGHLFCR"
63 a 222 c 217 g 123 t
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Homo sapiens mRNA for putative odorant binding protein ab (OBFIIa
                                                                                                   Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 725)

Pitior, G., Lacazette, E. and Gachon, F.

Polypeptides and polynucleotides coding for said polypeptides and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 CCIAGIGITCGGGAACGCAGCTICCCGTCTGCAGGGGGCGTGAAAATGTCCTCCTCCGAGA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 GTCCCTTGCGCTGCAACTTCTTAAATTCTTCCAGGGCCTCCCGGTTGGTATCAGAAT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 TCCTA------CCCACA 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 243.6; DB 6; Length 725;
Pred. No. 4.3e-57;
0; Mismatches 14; Indels 49
                                                                                                                                                                                                                            Patent: WO 0112806-A 3 22-FEB-2001;
Patent: WO Alvergue (FR); Pitiot, Gilles (FR)
Universite d'Auvergue (FR);
Location/Qualifiers
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AJ551022.1 GI:6900068
AJ511022.1 GI:6900068
GOBILA gene; odorant binding protein.
Homo sapiens.
AX083538 725 bp
Sequence 3 from Patent W00112806.
AX083538 AX083538.1 GI:13185348
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Best Local Similarity 83.2%;
Matches 311; Conservative (
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HSA251022/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative odorant binding protein a"
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             AJ251021

AJ251021

G1:6900066

OBPIJA gene; odorant binding protein.

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Primates; Catarrhini; Hominidae; Homo.

J. (Dases 1 to 676)

J. (Dases 1 to 676)

A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934; differential expression in the oral and
                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-00T-1999) Laboratoire de Biochimie Medicale - INSERM
1934, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
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Hum. Mol. Genet. 9 (2), 289-301 (2000)
20076326
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                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/chromosome="9"
/map="9934"
/map="9934"
/43.555
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1. .676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="OBPIIa"
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Gachon, A.M.
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AX083538/c
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                                                                                      ORGANISM
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HSA251023 607 bp mRNA linear PRI 02-FEB-2000 constant section and compared to putative odorant binding protein ad (OBPIIa
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IQRIWGQBAHIPALLEEFKKLVVQKGLGEEDIFNPLQTGSCVLEH"
197 c 172 g 104 t
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A novel human odorant-bloding protein gene family resulting from A novel human odorant-bloding protein gene family cons at 9934: differential expression in the oral and genital sphere.

Fun. Wol. Genet. 9 (2), 289-301 (2000)
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Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 607)
                                                                                                                                                                                             Pitiot, G., Lacazette, R. and Gachon, F. odorant-binding human proteins fixing hydrophobic ligands: polymeptides and polymucleotides coding for said polypeptides and uses thereof
                                                                                                                                     Homo sapiens
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota, Metazoa; Chordates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 60?)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43...486
/note="cDNRA396 (607) - forme courte (hOBPIIa-delta)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CTITATITIGGAGICAGGIGGGAGCAGGGAAGGGICAIGGCIGGAGGGIAGGICAG
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                                                                                                                                                                                                                                                                                                                                patent: WO 0112806-A 7 22-FEB-2001;
patent: WO 0112806-A 7 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Incoation/Qualifiers
I. 607
/Organism="Homo sapiens"
/db_xref="taxon:9606"
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#A7251023
A7351023.1 GI:6900070
OBFIIA gene; odorant binding protein.
Homo sapiens.
Sequence 7 from Patent W00112806.
                                  AX083542
AX083542.1 GI:13185352
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                                                                                                              human.
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Best Local Si
Matches 245;
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HSA251023/c
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ACCESSION
VERSION
KEYWORDS
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                                     Bukaryofs, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mamania; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 725)
1 acazette, E., Gachon, A.M. and Phtiot, G.
1 acozette, E., Gachon, A.M. and Phtiot, G.
2 a hovel human odorant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and genital spheres
                                                                                                                                                                                                                                                                                                           1 (bases 1 to 725)
2 (bases 1 to 725)
Gachon, A.M.
Gachon, A.M.
Blinet Submitssion
Submitted (26-007-1999) Laboratoire de Biochimie Medicale - INSERM
Submitted (26-007-1999) Laboratoire de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
1. 725
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Pred. No. 4.3e-57;
0; Mismatches 14; Indels 49;
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/db_xref="taxon:9606"
/chrcmosone="9"
/map="9434"
43. .483
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illarity 83.2%;
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                                                                                                                                                                                                                                       Query Match 70.8%; Score 238.6; DB 6; Length 741; Peet Local Similarity 96.4%; Prec No. 11e-55; Matches 244; Conservative 0; Mismatches 9; Indels 0;
                                               /note="CDNA396 (741) /SM4 (hOBPIIa-gamma)"
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/organism="Homo sapiens"
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43. .729
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Job time : 1104.85 secs
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229 C
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/protein_id=CaBri30.1"
/db.xef="d: 6900071"
/franslation="MKTLEFGTHGIAAALSFTLEEEDEGESVHPERPDAEDGAWO
IORIMGEALIPAAABGEKIALIOPPAFWGPALHGKAACGICSLGGRAAVPILAHLA
ISPAGNNPRINLEALEEFKKIVQRKGLSEEDIFPRFLQ7GSCVHSH"
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                                             Gachon, A.M.

Direct Valmission
Submitted (1207-1999) Laboratoire de Biochimie Medicale - INSERM
Submitted (207-1999) Laboratoire de Biochimie Medicale - INSERM
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
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1 (bases 1 to 741)
Pitot, G., Lacazette, E. and Gachon, P.
Odorant-binding human proteins fixing hydrophobic ligands:
Polypeptides and polynucleotides coding for said polypeptides and ses thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.3%; Score 240.2; DB 9; Length 607; Best Local Similarity 96.8%; Pred. No. 3.7e-56; Matches 245; Conservative 0; Mismatches 8; Indels 0;
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Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. .741
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Sequence 5 from Patent W00112806.
AXO83540 AXO83540.1 GI:13185350
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43. .486
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AX083540/c
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BS124; breast; cancer; detection; diagnosis; prevention; treatment;
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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AAH76463
AAS93598
AAQ69950
AAT35147
AAT35146
ABN43681
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ABA04115
ABA04103
AAF97910
ABA04107
ABA04111
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AAK51815
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AAS76054
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(ABBO ) ABBOTT LAB.
19-JUN-1998;
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133
129.8
78.8
74
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325
320.6
260.2
243.6
240.2
239.4
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 Human BS124 specif
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Gene No. 32 encodi
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Human PRO1283 prot
                                                                                     February 9, 2003, 19:57:40 ; Search time 123.814 Seconds
(without alignments)
6129.540 Million cell updates/sec
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| K.Geneseq_LJU1021;
| K.GENES/JCGddata/geneseqy-embl/Nk1981.bxf:*
| KIDSZ/JCGddata/geneseqy-embl/Nk1981.bxf:*
| KIDSZ/JCGddata/geneseqy-embl/Nk1983.bxf:*
| KIDSZ/JCGddata/geneseqy-embl/Nk1983.bxf:*
| KIDSZ/JCGddata/geneseqy-embl/Nk1985.bxf:*
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             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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AAX07456
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AAX08845
AAF54313
AAF58615
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Match Length
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Database :

New isolated BS124 polynucleotides and polypeptides - used for

WPI; 1999-105623/09.

Score

337 336.2 335.8 335.4 335.4

Degenerate lipocal Human reproductive Human reproductive Nuclectide sequenc ODNA corresponding The Accretion of Sequencial Programmer of Sequencia

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This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosing, monitoring, staging, imaging and treating breast cancer (BC). The methods comprise measuring the levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelied and used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TGGTATCAGAATTCCTACCACAAGCTTTCCCATGTGGAGCAGGCCCCCCATGGTGCTGGT 300
                                                                                                                                                                                                                                                                                                                                                     61 GGGTAGGTCCAGGTGGTCCGGGCTCTGTGTGTGGTAGGGTGGGCTCTGGAGGTGCAG 120
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                                                                                                                                                                                             Sequence 690 BP; 161 A; 208 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BS124 specific EST clone 1730294IH
            Example 1; Page 43; 45pp; English
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                                                                                                                                                                                                                                                                                                                  GGGTAGGTCCAGGTCCCGGGCTCTGTGTCTGGTGGTAGGGTGGCGCTCTGGAGGTGCAG 120
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                                                                                 The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                              Sequence 337 BP; 57 A; 80 C; 119 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast specific gene LS clone 1213903.
                                                    Claim 11; Page 94; 125pp; English.
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ID AAZ91770 standard; DNA; 690 BP.
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Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficidency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizopinenia; prostate disease; autoimmune disorder; AlbS; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CCICCICGAGAGICCCIIGCGCIGCACCAAITICIIAAAITCIICCAGGGCCICCCGGT 240
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                 New isolated BS124 polynucleotides and polypeptides - used for detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer
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                                                                                                         The sequence is that of a consensus BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                    Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CITIGCAGIAAAAGAIGIAGIGGICCCICCIGGGCAG 337
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AAVO8842/c
ID AAVO8842 standard; CDNA; 1002 BP.
                                                                                    Claim 11; Page 95; 125pp; English.
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97US-0044039.
97US-0048093.
97US-0048101.
97US-0048190.
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WPI; 1999-105623/09.
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30-MAY-1997;
30-MAY-1997;
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30-MAY-1997;
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                                    New isolated BS124 polynucleotides and polypeptides - used for detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                        Billing-medel PA, Cohen M, Colpitts TL, Friedman PN; Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD; Russell JC, Scheffel CP, Stroupe SD, Yu H;
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                                                                                                                                                                                                                                  100.0%; Score 337; DB 20; Length 692; 100.0%; Pred. No. 3.7e-87; ive 0; Mismatches 0; Indels 0.
                                                                                                                            The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                     Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BS124 specific EST clone consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CTTTGCAGTAAAAGATGTAGTGGTCCCTCCTGGGCAG 337
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                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 337; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consensus; ESI; ss
                 WPI; 1999-105623/09
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30-MAY-1997; 30-MAY-1997; 29-AUG-1997; 29-AUG-1997;

Carter KC,

Rosen CA,

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This sequence represents a cDNR of the invention, and is designated cane No. 32. This sequence encodes a human secreted protein, and is expressed primarily in endometrial tumour.

Expressed primarily in endometrial tumour.

Corresponding secreted to the invention and their corresponding secreted protein by a sequences of the invention and their corresponding secreted polymetrides are useful for preventing, treating or ameliorating medical conditions.

Correlation and protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polymetrides in a sample or by determining the presence of mutations in the DNR sequences. Sample or by determining the presence of mutations in the DNR sequences. Secretic uses are described for each of the DNR sequences and the encoded proteins, based on which tissues they are most highly expressed in, and proteins, based on which tissues they are most highly expressed in, and citized developing products for the diagnosis or treatment of cancer chumours, neurological disorders, leukaemiss, diseases of the immune system citization and Albs: the polypeptides are also useful for identifying the contract of the polypeptides are also useful for identifying
                                                                                           Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abrormality; foctal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; Alb6; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental disorders or blood disorders
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99.6%; Score 335.8; DB 2
Best Local Similarity 99.1%; Pred. No. 9.2e-87;
Matches 334; Conservative 3; Mismatches 0
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                                                                  Gene No. 32 encoding human secreted protein.
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970S-0044039.
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                 19-FEB-1999 (first entry)
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Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                        Homo sapiens.
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29-AUG-1997;
29-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a cDNR of the invention, and is designated concerns. This sequence encodes a human secreted protein, and is expressed primarily in endometrial tumour. Concerns the protein and is expressed primarily in endometrial tumour. Concerns the plan sequences of the invention and their corresponding secreted protein by sequences of the invention and their corresponding secreted colling to an endometrial protein or gene therapy. Also pathological conditions concerns by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNR sequences. Specific uses are described for each of the DNR sequences and the encoded corporate products for the diagnosis of treatment of cancer include developing products for the diagnosis or treatment of cancer tumours, neurological disorders, developmental abnormalities and foetal disorders, allowables, diseases of the immune system cliniding allorides or asthma, hepatic disease, Alzheimer's and consistent consistent consistent consistent and AIDS. The polypeptides are also useful for identifying the consistence of the polypeptides are also useful for identifying the consistence of the polypeptides are also useful for identifying the consistence of the 
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Pred. No. 7.1e-87;
2; Mismatches 0; Indels 0;
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                                                                                                                                                                                  Feng P,
                                                                                                                                                                                    Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 139; 188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.8%;
        97US-0048356.
97US-0050935.
97US-0056250.
97US-0056293.
                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                Dillon PJ, Engra
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Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                their binding partners.
                                                                                                                                                                                                              Ruben SM,
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P-PSDB; AAW73428.
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Query Match

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AAV08845;

RESULT 6
AAV08845/c
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Human; immune related disease; diagnosis; antiinflammatory; cardiant;
Wearmatological, antiarthritis; antirheumatic; immunosuppressive;
Wearmatological, antiarthritis; antiantopic; neuroprotective;
mutianemic; hepatorropic, virucide; antiportatic, antiallargic;
mutiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
We stecarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW systemic vasculitis; autoimmune haemolytic anaemais; diabetes mellitus;
We atoimmune thrombooytopaenia; immune-mediated renal disease;
Milammatory bowel disease; luten-sensitive enteropath;
Milammatory bowel disease; luten-sensitive enteropath;
Milammatory bowel disease; iquten-sensitive enteropath;
Milammatory and disease; immune-mediated skin disease; alleryic disease;
Milammatory disease; immune-mediated skin disease; sileryic disease;
Milammatory disease; immune-mediated skin disease; sileryic disease;
Milammatory disease; host-disease; ss.
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                                                                                                                                                                                                                                                    121 ACCCGGGGGCTGCCTAOTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGGGGTGTAAATGT 180
                                                                                                                                                                                                                                                                                         511
                                                                                                                                                                                                                                                                                                                                                                                                241 TGGTAICAGAAITCCIACCCACAAGCTIICCCAIGTGGAGCAGGCCCCCAIGGIGCIGGI 300
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                      1 GGGGGAGAAGGACTTTATTTGGAGTCAGGTGGGTGGGAGCAGGGAAGGGTCATGGCTGGA 60
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                               99.5%; Score 335.4; DB 22; Length 738; ilarity 99.7%; Pred. No. 1.1e-86; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO1283 protein UNQ653 encoding cDNA SEQ ID NO:169.
Sequence 738 BP; 209 A; 207 C; 205 G; 117 T; 0 other;
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AAC58615/c
ID AAC58615 standard; cDNA; 739 BP.
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9905-0123957.
9905-012575.
9906-0128849.
9906-0131445.
9905-0131371.
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                                                          Best Local Similarity
Matches 336; Conserv
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10-MAR-1999;
12-MAR-1999;
23-MAR-1999;
23-MAR-1999;
28-APR-1999;
04-MAY-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fong S;
Hillan KJ;
                                                                                                                                                                                              121 ACCCGGGGGCTGCCTAGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAAATGT 180
                                                                           CCTCCTCGAGAGTCCCTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGT 240
                                                                                                                                              897 GGGTAGGTCCAGGTGCTGGGCTCTGTGTCTGGTAGGGTGGGCTCTGGAGGTGCAG 838
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                                                                                                                                                                                                                                                                             301 CTTTGCAGTAAAAGATGTAGTGGTCCCTCCTGGGCAG 337
                                                                                                                                                                                                                                                                                                      DNA encoding protein of the invention #50.
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20-JUL-1999; 99US-0144756.
26-JUL-1999; 99US-015568.
01-SEP-1999; 99WC-01520111.
02-DC7-1999; 99WC-US28131.
02-DC7-1999; 99WC-US28131.
02-DC7-1999; 99WC-US28531.
05-DC7-1999; 99WC-US28531.
05-DC7-1999; 99WC-US20095.
06-JAN-2000; 2000WC-US00219.
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ID AAF54313 standard; DNA; 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
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241 rggratcagaatrccraccacacaagcttrcccargragcagcccccarggracraggr 300
                                                                                                                                                                                                                                                                                                                            Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
                                                                               121 ACCCGGGGCCTGCCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGCGTGAAATGT
                                                                                                                                                                                                                        181 CCICCICCGAGAGICCCITGCGCIGCACCAAITICITAAAITCTICCAGGGCCICCCGGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CITIGCAGIAAAAGAIGIAGIGGICCCICCIGGGCAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 CITTGCAGIAAAGAIGTAGTGGTCCCTCCTCGGCAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    071/c
AAA37071 standard; cDNA; 739 BP.
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98US-0098749.
98US-0098750.
98US-0098803.
98US-0098813.
98US-0098843.
98US-0099536.
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98US-0099792.
98US-0099808.
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02-SEP-1998;
02-SEP-1998;
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09-SEP-1998;
09-SEP-1998;
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10-SEP-1998;
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15-SEP-1998;
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CC AACG8397 to AACS857 perpesent PoR primers and hybridisation probes used in the isolation of human PRO sequences. AACS879 to AACS847 represent human PRO polymnological disease and profess the control control and praft-versus-incr-disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W; Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V; Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
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99WO-US28313.
99WO-US28409.
99WO-US28301.
99WO-US28634.
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2000WO-US00277.
2000WO-US00376.
2000WO-US03565.
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99WO-US28564.
99WO-US30095.
99WO-US30999.
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P-PSDB; AAB33450.
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01 - DBC - 1999;
02 - DBC - 1999;
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16 - DBC - 1999;
30 - DBC - 1999;
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30 - DBC - 1999;
16 - JAN - 2000;
17 - JAN - 2000;
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29 - OCT - 1999
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98US-0100662 98US-0100664

16-SEP-1998; 16-SEP-1998; 16-SEP-1998; 16-SEP-1998;

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9805 - 0.105694
9805 - 0.105694
9805 - 0.105887
9805 - 0.106062
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980S-0103401.
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980S-0104257.
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98US-0106902.
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980S - 0102687.
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980S - 0103965.
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9805 - 0100683 . 9805 - 0100684 . 9805 - 0100710 . 9805 - 0100711 . 9805 - 010093 . 9805 - 010093 . 9805 - 010093 . 9805 - 010074 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 010177 . 9805 - 01017 . 9805 - 01017 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 . 9805 - 010727 .
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98US-0105693
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14-0CT-1998;
20-0CT-1998;
21-0CT-1998;
21-0CT-1998;
22-0CT-1998;
22-0CT-1998;
23-0CT-1998;
27-0CT-1998;
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28-0CT-1998;
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28-0CT-1998;
28-0CT-1998;
28-0CT-1998;
29-0CT-1998;
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01-OCT-1998;
01-OCT-1998;
02-OCT-1998;
06-OCT-1998;
07-OCT-1998;
07-OCT-1998;
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29-SEP-1998;
30-SEP-1998;
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30-SEP-1998;
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23-SEP-1998;
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23-SEP-1998;
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24-SEP-1998;
                                                      17-SEP-1998;
18-SEP-1998;
18-SEP-1998;
18-SEP-1998;
18-SEP-1998;
18-SEP-1998;
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23-SEP-1998;
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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential perital cor small nolecule inhibitors of the relevant receptor/ligatide or small nolecule inhibitors of the relevant encogency/ligatid interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmacentical and diagnostic agents. AAA37145 to AAA37330 represent pCR primers and hybridatation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                         New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCICCICCGAGAGICCCIIGCGCIGCACCAAITICIIAAAITCIICCAGGGCCICCCGGI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGGIAGGICCAGGIGCICCGGGCICTGIGGIGGIAGGGIGGGCICTGGAGGIGCAG 120
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                                                                                                                                                                                                                                                                                                  Wood
                                                                                                                                                                                                                                                                                                 Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                  Smith V,
                                                                                                                                                                                                                                                                                                     Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 99; 773pp; English.
         9805 - 0106919.
9805 - 0106914.
9805 - 0106914.
9805 - 0108178.
9805 - 0108179.
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                                                                                                                                                                                                                                                                                                      Baker K, Goddard A,
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P-PSDB; AAY99389.
03-NOV-1998;
03-NOY-1998;
03-NOY-1998;
10-NOY-1998;
17-NOY-1998;
17-NOY-1998;
17-NOY-1998;
17-NOY-1998;
17-NOY-1998;
17-NOY-1998;
17-NOY-1998;
18-NOY-1998;
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301 CTTTGCAGTAAAAGATGTAGTGGTCCCTCCTGGGCAG 337

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
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T, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothellal or angiogenic disorders in a mammal -
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 205; 567pp; English.
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(PAON) PAONI N F.
(STEP) STEPHAN J F.
(WALL) NATANABE C K.
(WALL) WOOD W I.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                               WPI; 2002-171999/22.
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                                                                                                                                                                                                                                        Stephan JF,
                                                                                                                                                                                                Baker KP,
    (HILL/)
(MARS/) |
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                                                                                                                                                                                                                                                                Human angiogenesis related cDNA PRO1283 SEQ ID NO: 205
       390 CTTTGCAGTAAAGATGTAGTGGTCCCTCCTCGGCAG 354
                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2000; 2000US-219556P.
25-JUL-2000; 2000US-220654P.
28-JUL-2000; 2000US-220654P.
28-JUL-2000; 2000US-220659P.
17-AUG-2000; 2000US-22069P.
17-AUG-2000; 2000US-0543557.
24-AUG-2000; 2000US-054357.
24-AUG-2000; 2000US-054358.
07-SEP-2000; 2000US-200978P.
18-SEP-2000; 2000US-050928.
18-SEP-2000; 2000US-050928.
24-CCT-2000; 2000US-0564510.
24-CCT-2000; 2000US-0564510.
24-CCT-2000; 2000US-0564510.
26-NOY-2000; 2000US-0564510.
26-NOY-2000; 2000US-0564510.
26-DEC-2000; 2000US-0564510.
26-DEC-2000; 2000US-05656.
26-PER-2001; 2001US-05666.
26-PER-2001; 2001US-0566.
26-PER-2001; 2001US-0560.
26-PER-2001; 2001US-0566.
26-PER-2001; 2001US-0566.
26-PER-2001; 2001US-0566.
26-PER-2001; 2001US-056.
                                                                                                                            i663/c
ABL95663 standard; cDNA; 739
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GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
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FERRARA N.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                              19-JUL-2002
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ABL95663
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Gaps

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Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthms; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; Ss.
e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atheroscierosis, hypertension, arterial restenosis, rhemancoid arthritis, andriam, mycoardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymoiceotides have applications in nolecular blotogy, including use as hybridisation probes, and in chromosome and gene mapping. Rables259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                              61 GGGTAGGTCCAGGTGCTCCGGGCTCTGTGTGTGGTAGGGTGGGGCTCTGGAGGTGCAG 120
                                                                                                                                                                                                                                                                                                121 ACCCGGGGGCTGCCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAATGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a /*tag= a /*tag= a polypeptide OBPIIb-gamma"
                                                                                                                                                                                                                                       1 GGGGGAGAAGGACTTTATTGGAGTCAGGTGGGTGGGAGCAGGGAAGGGTCATGCCTGGA 60
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                                                                                                                                                                                                                                                                                                                                                           181 CCTCCTCCGAGAGTCCCTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of odorant binding polypeptide OBPIIb-gamma.
                                                                                                                                                                99.5%; Score 335.4; DB 24; Length 739; 99.7%; Pred. No. 1.1e-86; tive 0; Mismatches 1; Indels 0;
                                                                                                                                     Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
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43..300
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                                                                                                                                                                          Query Match
Best Local Similarity 99.7
Matches 336; Conservative
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(PIII/) PITIOT G.
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                    vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; dendochalial disorder; cancer; andiogenic disorder; candiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rhemactoi arthritis; mycoradial inffarction; thrombophlebitis; lymphanyliis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Te W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 205; 565pp; English.
                                                                                                                                                                                                                                                        23-JUTN-2000; 2000US-213637P.
25-JUL-2000; 2000US-21056F.
25-JUL-2000; 2000US-220664P.
25-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-0643657.
23-AGG-2000; 2000US-0643522.
24-AGG-2000; 2000US-0643522.
24-AGG-2000; 2000US-0643657.
24-AGG-2000; 2000US-0643528.
24-AGG-2000; 2000US-065350.
18-SEP-2000; 2000US-065350.
18-SEP-2000; 2000US-065350.
28-PEP-2000; 2000US-065350.
20-DEC-2000; 2000US-US30873.
20-DEC-2000; 2000US-US30873.
20-DEC-2000; 2000US-US30873.
20-DEC-2000; 2000US-US34956.
22-JAN-2001; 2001US-0767609.
22-JAN-2001; 2001US-0767609.
22-JAN-2001; 2001US-0767609.
23-MAR-2001; 2001US-0808689.
25-MAR-2001; 2001US-0808689.
25-MAR-2001; 2001US-0808689.
25-MAR-2001; 2001US-0808689.
25-MAR-2001; 2001US-0864208.
25-MAR-2001; 2001US-0866034.
25-MAR-2001; 2001US-0866034.
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2001WO-US17443.
2001WO-US17800.
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P-PSDB; ABB84919.
                                                                                                                                                                        WO200200690-A2.
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(UYAU-) UNIV AUVERGNE. (PITI/) PITIOT G.
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                                                                                                                              WO200112806-A2.
               Homo sapiens.
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                                                                                                                                                         The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPID-gamma (short form). OBPs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc. OBP polypeptides are used as binding proteins (perfumes, deodorants etc.) as competitive compounds as competitive compositions (aponists or antagonists) of cellular lipocalcin receptors; inhibitors (aponists or antagonists) of cellular lipocalcin receptors; concert specific antibodies for diagnosis of allergy, asthma or cancer; commeties or disinfectant compositions; to screen compounds, especially comments or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; or treating hyperlipidemia or obesity, or to supplement non-maternal anily when combined with nutritional fatty acids, as food additives; as a conflayed release) but also for delayed release) but also for delayed across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or contagnosing deducing an ample of the amniotic membrane); and as antiallergic agents.
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                                                              New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.4%; Score 325; DB 22; Length 542; Best Local Similarity 100.0%; Pred. No. 9.8e-84; Matches 325; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 542 BP; 129 A; 169 C; 155 G; 89 T; 0 other;
                                                                                                                                       Claim 6; Page 117-118; 132pp; French.
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                     WPI; 2001-202864/20.
P-PSDB; AAB67744.
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The present sequence encodes a human odorant binding polypeptide (OBP), costinated OBFID-alpha. OBPS provide long-term retention (gradual designated OBFID-alpha. OBPS provide long-term retention (gradual compounds, so prolong the hold of perfumes, relates) of lipophilito compounds so prolong the hold of perfumes, competitise to. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors for specific antibodies for diagnosis of allergy, asthma or cancer; for specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, controlling volatilisation of an odorant, specifically in perfumes, compounds, especially concounts or flavours. e.g. human pheromones, for binding to OBP, also in controlling when compounds, or obesity, or to supplement non-maternal for treating hyperlipidema or obesity, or to supplement non-maternal antibute or transporter of pharmaceuticals, especially anticancer agents (providing compounds release) but also for delivery across the placental barrier (e.g. for decoilation) of the foetus); as a marker of pregnancy or contained archifolds, repeated and present of pregnancy or contained archifolds.
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/product= "odorant binding polypeptide OBPIIb-alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 113-114; 132pp; French.
Location/Qualifiers
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Best Local Similarity 100.
Matches 325; Conservative
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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBFIra-alpha. OBFs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
                                                                                                                                                                                                                                                                                                                            253 TCCTACCCACAAGCTTTCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAA 312
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Indels
    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  482 AGAIGIAGICCCICCIGGGCAG 458
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      Matches 325; Conservative
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AAF80039/
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                436 TCCTACCCACAAGCTTTCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAA 377
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/product= "odorant binding polypeptide OBPIIb-beta"
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AAF80044 standard; cDNA; 782
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P-PSDB; AAB67743.
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Best Local Similarity
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deodorants etc.. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lippoaloin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in partimes, constituent of disinfectant compositions; to screen compounds, especially codorants or flavours, e.g. human pheromones, for binding to OBP, also in the treating hyperlipidemia or obesity, or to supplement non-maternal for treating hyperlipidemia or obesity, or to supplement non-maternal can mix when combined with nutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticenter agents (providing diagred release) but also for delivery across the placental barrier delayed release) but also for delivery across the placental barrier of e.g. for detoxification of the foctus); as a marker of pregnancy or contain particular of the foctus;
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Best Local Similarity 95.7
Matches 311; Conservative
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Scoring table:

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Sequence 6, Appli
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   3 US-08-510-646B-6
4 US-09-518-18-6
4 US-09-165-264-8
1 US-08-232-463-14
4 US-09-276-531-1
4 US-09-276-531-1
1 US-08-437-4(7)-9
1 US-08-447-96-17
4 US-09-641-658-23
4 US-09-641-638-23
4 US-09-65-76-64
3 US-08-814-095-7
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; Sequence 1, Application US/09130653A
; Barlane 1, No. 6020163
; GENERAL INFORMATION:
    APPLICAMY: CORMIN, Darrell C,
    TITLE OF INVENTION: LIPOCALIN HOMOLOG
    TITLE OF INVENTION: LIPOCALIN HOMOLOG
    CURRENY APPLICATION NUMBER: US/09/130,663A
    CURRENY FILING DATE: 1998-08-05
    CURRENY FILING DATE: 1997-08-06
    NUMBER OF SEQ ID NOS: 30
    SOFTWARE PARISEZ for Windows Version 3.0
    SEQ ID NO 1
    LENGTH: 522
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1S-09-432-335-1/c

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Patent No. 6145720

PAPLICANT: CORKIION:

APPLICANT: CORKIION:
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1955 4
41155 4
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318 4
3506 3
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ORGANISM: Homo sapiens
FEATURE:
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US-09-130-663-1/c
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Sequence 1, Appli
Sequence 28, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 20, Appli
                                                                                                                                    ; ; Search time 24.4956 Seconds (without alignments) 4219,129 Million cell updates/sec
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337
1 GGGGGAGAAGGACTITATIT......IAGTGGTCCCTCCTGGGCAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/AB_COMB.seq:*
/cgn2_6/ptodata/1/ina/AB_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-09-614-022-1

08-09-130-653-5

08-09-432-335-5

08-09-410-022-5

08-08-466-793-1

08-09-411-861A-1

08-09-411-861A-1

08-09-4130-663-17

08-09-432-335-17

08-09-432-335-19

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08-09-432-335-19

08-09-432-335-19

08-09-432-335-19

08-09-432-335-19

08-09-432-335-19

08-09-432-335-19

08-09-432-335-10

08-09-432-335-10

08-09-432-335-10

08-09-486-240-3

08-08-765-907A-1

08-08-765-907A-1
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            February 9, 2003, 20:30:25
                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                   IDENTITY_NUC Gapext 1.0
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Maximum DB seg length: 200000000
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Query
Match ]
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Perfect score:
Sequence:
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                                                                                                            0; Gaps
197 CTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGGTGGTATCAGAATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Degenerate sequence derived from human zlipol OTHER INFORMATION: nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 43.6%; Score 147; DB 3; Length 510; Best Local Similarity 57.7%; Pred. No. 2.3e-34; Matches 116; Conservative 53; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                         RESULT 4
US-09-130-663-5/C
US-09-130-663-5/C
Sequence 5, Application US/09130663A
Patent No. 6020163
Sequence 5, Application US/09130663A
FAREAL THORORATION:
TITLE OF INVENTION LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130,663A
CURRENT PILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER PILING DATE: 1998-08-05
SOFTWARE: FAREACATION NUMBER: 60/054,867
SARLIER FILING DATE: 1998-08-05
SOFTWARE: FASTERO FOR MINGENE: 60/054,867
SOFTWARE: FASTERO FOR NOS: 30
SOFTWARE: FASTERO FOR WINDOWS VERSION 3.0
SURVEY.
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19-09-432-335-5/c
5 Sequence 5, Application US/09432335
7 Patent No. 6143720
7 SEGNERAL INPORMATION:
APPLICANT: CONKIN, Darrell C.
TILLE OF INVENTION: LIPOCALIN HOMOLOG
CURRENT APPLICATION NUMBER: US/09/432, 335
CURRENT PILING NATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
FARLIER FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: variation
LOCATION: (1)...(510)
COTHER INYORWATION: n is any nucleotide
US-09-130-663-5
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.6%; Score 201; DB 3; Length 522; Beet Local Similarity 100.0%; Pred. No. 2.6e-50; Matches 201; Conservative 0; Mismatches 0; Indels
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Sequence 1, Application US/09614022

Patent No. 636516

SERVERAL INFORMATION:

TITLE OF INVENTION: LIPCOALIN HOMOLOG

TITLE OF INVENTION: LIPCOALIN HOMOLOG

TITLE OF INVENTION: LIPCOALIN HOMOLOG

PRIOR APPLICATION NUMBER: US/09/614,022

CURRENT FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 09/130,663

PRIOR PELLING DATE: 1998-08-06

PRIOR PELLING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 30

SOFTWARE PRAISE PRAISE 1998-08

SOFTWARE PRAISE PRAISE 1998-08

SEQ ID NO 1

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PROSE IN NO 1

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PROSE IN NO 1

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PROSE IN NOS: 30
          TITLE OF INVENTION: LIPOCALIN HOMOLOG
OURRANT APPLICATION NUMBER: US/09/432,335
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
BARLIER APPLICATION NUMBER: 09/130,663
BARLIER APPLICATION NUMBER: 06/054,867
BARLIER APPLICATION NUMBER: 60/054,867
BARLIER APPLICATION NUMBER: 60/054,867
SARLIER APPLICATION NUMBER: 05/054,867
SARLIER FILING DATE: 1997-08-06
NUMBER OF SED ID NOS: 30
SOFTHARE: FASLERQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 GTAGTGGTCCCTCCTGGGCAG 316
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (7)...(516)
US-09-614-022-1
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; NAME/KEY: CDS
; LOCATION: (7)...(516)
US-09-432-335-1
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257 ACCCACAGGTTTCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAAGAT 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Morgenstern, Jay P.
APPLICANT: Manieczny, Andrzey
APPLICANT: Biaindaukas, Christine B.
APPLICANT: Biaindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergeanic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor WUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMI-026CP(IPC-048CP)
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STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
PRICR APPLICATION DATA:
APPLICATION UNMBER: US/08/156,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: APPLICATION NUMBER: 07/999,712
                                                                                                                                                                                                                                                                                                                                                                                   US-08-467-603-1/c
Sequence 1, Application US/08467603
Patent No. 5843672
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-Dec-92
ATTORNER FAGERT INFORMATION:
NAME: MEGISTRATION UNDERS: 36,207
REFERENCE/DOCKET NUMBER: 1MI-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-741
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERICATICS:
LEMNTH: 525 base pairs
TERENTH: 525 base pairs
TERENTH: 625 base pairs
                                                                                                                                                                                                                                        317 GTAGTGGTCCCTCCTGGGCAG 337
                                                                                                                                                                                                                                                                   330 RTARTGRTCNCKNCKNGGNAR 310
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Best Local Similarity 64.69
Matches 126; Conservative
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LOCATION: 1..525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boston
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US-08-467-603-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Degenerate sequence derived from human zlipol
                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 13; Score 147; DB 3; Length 510; Local Similarity 57.7%; Pred. No. 2.3e-34. Indels les 116; Conservative 53; Manatches 32; Indels les 116; Conservative 53; Manatches 32; Indels
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// Sequence 5, Application US/09614022

// Sequence 5, Application US/09614022

// Sequence 5, Application US/09614022

// SENERAL INFORMATION:

// TYLE APPLICATION:

// TYLE OF INVERTION: LIPCCALIN HOWOLOG

// TYLE OF INVERTION: 97-94

CURRENT APPLICATION NUMBER: US/09/614,022

CURRENT FILING DATE: 2000-07-11

// PRIOR PAPLICATION NUMBER: 09/130,663

// PRIOR PALING DATE: 1998-08-06

// PRIOR PAPLICATION NUMBER: 09/130,663

// PRIOR PAPLICATION NUMBER: 1997-08-06

// NUMBER OF SEQ ID NOS: 30

// SOFTWARE TESTER OF WINDOWS VERSION 3.0

// SEQ ID NO 5

LENGTH: 510
EARLIER APPLICATION NUMBER: 60,054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PRSTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                           ; NAME/KEY: variation
; LOCATION: (1)...(510)
; OTHER INFORMATION: n is any nucleotide
US-09-43z-3335-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KET: variation

// LCCATION: (1)...(510)

OTHER INFORMATION: n is any nucleotide

US-09-614-022-5
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                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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140 TICGGGAACGCAGCTICCCGTCIGCAGGGGCGTGAAAATGTCCICCTCCGAGAGTCCCTT 199
    Query Match 21.8%; Score 73.4; DB 2; Length 525; Best Local Similarity 64.6%; Pred. No. 1.26-12; Matches 126; Conseryative 0; Mismatches 66; Indels 3; Gaps
                                                                                                                                                                                                                  516 rccresasascaserrrcscreresessarrccaaaarcresegre---aarcerr 460
                                                                                                                                                                                                                                                                                         200 GCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGTTGGTATCAGAATTCCTACC 259
                                                                                                                                                                                                                                                                                                                                                             459 GGCTCTTGAGAATTCCCGGAAATCCTCCAAGGCCTCTTGGCTCTGGCTCAGGATCCCTTCC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                    260 CACAAGCTTTCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAAAGATGTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-491-861A-1/C
| Sequence | Application US/08491861A |
| Sequence | Application US/08491861A |
| Patent No. 59323B |
| CENERAL INFORMATION: |
| APPLICANT: Morgenstern, Jay P. |
| APPLICANT: Maiccony, Andreay |
| APPLICANT: Bilandankas, Christine B. |
| APPLICANT: Branch Andrew W. |
| TITLE OF INVENTION: Dander and Uses Therefor |
| NUMBER OF SEQUENCES: 104 |
| NUMBER OF SEQUENCES: 104 |
| APPLICANT: ALAITYE & COCKTEILD, ILP |
| CORRESPONDENCE ADDRESSS: |
| ADDRESSEE: ALAITYE & COCKTEILD, ILP |
| CORPERIOR OF SEQUENCES |
| CORPERIOR OF SEQUENCES |
| CONTRESPONDENCE ADDRESSES: |
| ADDRESSEE: ADDRESSEE: |
| ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMI-026CP(IPC-048CP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY GISK
MEDIUM TYPE: FLORPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GOFTWARE: ASCIL-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,861A
FILING DATE: 27-007-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
ANNOWAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAME: Mandraguras, Any E.
REGISTRATON NUMBER: 36,207
REPERBONCPOCKET NUMBER: IM-COMMUNICATION INDEPEN: IM-COMMUNICATION INDEPEN: IM-COMMUNICATION INDEPEN: (617) 242-4214
INDEPENSION SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 GTGGTCCCTCACCGG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 GTGGTCCCTCCTGGG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
140 TICGGGAACGCAGCINCCCGTCIGCAGGGGCGTGAAAAGTGTCCTCCTCCGAGAGTCCCTT 199
                                     459 GGCTCTTGAGAATTCCCGAAAATCCTCCAAGGCCTCTTGGCTCTGCTCAGGATCCCTTTC 400
                                                                                                                                                                                                                                                                                                                       199 CAGAAGCTTGGCCATTCGGATCTGCCTCCCATGGACCTCGCCTCGCAGTAGAGAATGTA 340
                                                                                                                                      200 GCGCTGCACCAATITCTTAAATTCTTCCAGGGCCTCCCGGTTGGTATCAGAATTCCTACC 259
                                                                                                                                                                                                                                                                                 260 CACAAGCTTTCCCATGTGGAGCAGGCCCCCATGGTGGTGGTGTTTGCAGTAAAAGATGTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Morgenstern, Jay P.
APPLICANT: Rahieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W
TITLE OF INVENTION: Allergemic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mandragouras, Awy E.
REGISTRATION NUMBER: 36,207
REFERENCE/POCKET NUMBER: IMI-026CP(IPC-048CP)
THECOMMUNICATION INFORMATION:
THELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
MEDIUM TYEE: Floppy disk
COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIT-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,793
FILING DATE: 06-JUN-1995
CLASSIFFICATION NUMBER: US/08/156,549
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATJONEDY AGGNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 525 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                            320 GIGGICCCICCIGGG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 GIGGICCCICACCGG 325
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; LOCATION: 79..525
US-08-466-793-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 1..525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH:
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136 AGIGITCGGGGAACGCAGCTTCCCCGTCTGCAGGGGCGTGAAATGTCCTCCTCCTCCGAGAGTC 195
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                                                                                                                                                                                                                                                                                                19.4%; Score 65.4; DB 3; Length 147; 98.5%; Pred. No. 1.8e-10; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%; Score 65.4; DB 4; Length 147; 98.5%; Pred. No. 1.8e-10; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL IMPOGMATION:
APPLICANT: CORALIA, DARRALI C.
FILTE OF INVENTION: LIPOCALIN HOMOLOG;
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130,663A
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,967
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESTE OF WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 17; LENGTH: 147
                                                                                                                   ; OTHER INFORMATION: C-terminal 3' linker US-09-432-335-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: C-terminal 3' linker US-09-614-022-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09130663A Patent No. 6020163
                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                           Best Local Similarity 98.5
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.59
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                           196 CCTTGCG 202
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US-09-130-663-19/c
                                                                                                                                                                                            Query Match
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                                                                                                                       140 ITCGGGAACGCAGCTTCCCGTCTGCAGGGCGTGAAAATGTCCTCCTCCGAGAGTCCCTT 199
                                                                                                                                                                                                        200 GCGCIGCACCAATITCTIAAAITCTICCAGGGCCICCCGGTIGGTATCAGAATTCCTACC 259
                                                                                                                                                                                                                                                                                         260 CACAAGCITICCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAAAGATGTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 AGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAAATGTCCTCCTCCGAGAGTC 195
                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGAGTGAAAATGTCCTCCTCCAGAAGTC 8
                                       Query Match 21.8%; Score 73.4; DB 2; Length 525; Best Local Similarity 64.6%; Prect. No. 128-12; Matches 126; Conservative 0; Mismatches 66; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 19.4%; Score 65.4; DB 3; Length 147; Local Similarity 98.5%; Pred. No. 188-10; Lesson 66; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09130663A
; Patent No. 6020163
; Patent No. 6020163
; Fatent No. 6020163
; TITLE OF INVENTION: LIPOCALIN HOMOLOG
; TITLE OF INVENTION: LIPOCALIN HOMOLOG
; FILE REFERENCE: 97-24
; CURRENT PILING DATE: 199-08-05
; EARLIER APPLICATION NUMBER: 06/054,867
; EARLIER PILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FRASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DARE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / FEATURE:
/ OTHER INFORMATION: C-terminal 3' linker
US-09-130-663-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: CORALIN, DATEAL C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09432335; Patent No. 6143720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     339 GIGGICCCICACCGG 325
                                                                                                                                                                                                                                                                                                                                                                          320 GIGGICCCICCIGGG 334
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US-09-130-663-17/c
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US-08-491-861A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Best Local Similarity 98.0%; Pred. No. 6.2e-06;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.7%; Score 49.4; DB 3; Length 51; Best Local Similarity 98.0%; Pred. No. 6.2e-06; Matches 50; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Oligonucleotide primer: ZC13727
US-09-432-335-19
                                                                                                                                                                                                                     RESULT 14

US-09-432-335-19/C
US-09-432-335-19/C
Sequence 19, Application US/09432335
Patent No. 6143720
SCHERAL INFORMATION:
TITLE OF INVENTION: LIPOCALIN HOMOLOG
TITLE OF INVENTION: LIPOCALIN GOMOLOG
CURRENT PILLING DATE: 1999-11-02
EARLIER PILLING DATE: 1999-11-02
EARLIER PILLING DATE: 1998-08-06
EARLIER FILLING DATE: 1998-08-06
SARLIER FILLING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRALEQ FOR MINGOWS VERSION 3.0
SOFTWARE: FRALEGO FOR MINGOWS VERSION 3.0
EARLIER PILLING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRALEGO FOR MINGOWS VERSION 3.0
EARLIER PILLING DATE: 1997-08-06
ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-614-022-19/C
Sequence 19, Application US/09614022
Fatent No. 6365716
Fatent No. 6365716
FAREAL INFORMATION:
TITLE OF INVENTATION:
TITLE OF INVENTATION: LIPOCALIN HOMOLOG
FILE REPERENCE: 97-24
CURREMY FILING DATE: 2000-07-11
FRIOR PILING DATE: 1998-08-06
FRIOR FILING DATE: 1998-08-06
FRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ. ID NOS: 30
SOFTWARE FRASEQ for Windows Version 3.0
LENGTH: 51
                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                     SEQ ID NO 19
LENGTH: 51
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; FEATURE; ;- OTHER INFORMATION: Oligobucleotide primer: 2C13727

TYPE: DNA ORGANISM: Artificial Sequence

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0; Gaps
Query Match 14.7%; Score 49.4; DB 4; Length 51, Best Local Similarity 98.0%; Pred. No. 6.2e-06; Matches 50; Conservative 0; Mismatches 1; Indels Matches 50; Conservative 0; Mismatches 1;
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Search completed: February 9, 2003, 22:05:13 Job time: 32.4956 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																			,
Description	Sequence 3, Appli	Sequence 803, App	Sequence 4, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 25, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 37, Appl	Sequence 9, Appli	Sequence 17, Appl		Sequence 237, App	Sequence 237, App	Sequence 237, App		Sequence 37, Appl	Sequence 53, Appl
ΩI	US-09-099-823-3	US-09-833-381-803	US-09-099-823-4	US-09-099-823-5	US-09-951-845-1	US-09-374-671-1	US-09-854-847-25	US-10-143-576-1	US-09-854-847-1	US-09-800~729-37	US-09-854-847-9	US-09-854-847-17	US-10-028-072-237	US-10-121-049-237	US-10-123-904-237	US-10-140-470-237	US-09-878-574-4330	US-09-880-192-37	US-09-822-830A-53
DB	10	10	10	10	10	10	10	6	10	10	10	10	σ	σι	σ	g	10	10	10
* Query Match Length DB ID	337	501	692	692	523	525	432	555	555	570	579	597	762	762	762	762	504	3502	1434
% Query Match	100.0	100.0	100.0	100.0	59.6	21.8	13.2	13.2	13.2	13.2	13.2	13.2	12.8	12.8	12.8	12.8	11.3	10.7	10.6
Score	337	337	337	337	201	73.4	44.6	44.6	44.6	44.6	44.6	44.6	43	43	43	43	38.2	36.2	35.6
Result No.	~ I	7	ო	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19
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ALIGNMENTS

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RESULT 1

Sequence 3, Application US/0909823

APPLICANT: COHEN, MUNICES

APPLICANT: COLPITS, TRACET L.
APPLICANT: GCREON, MULLAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: REASC, MICHAEL R.
APPLICANT: REASC, MICHAEL R.
APPLICANT: REASC, MICHAEL R.
APPLICANT: REASC, MICHAEL R.
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: REASCHING DISEASES OF THE BREAST
TITLE OF INVENTION: REAGENERS AND METHODS USEFUL
TITLE OF INVENTION: REAGENERS AND METHODS USEFUL
APPLICANT: ADDOCT PAIK ROAD
TITLE OF INVENTION: REAGENERS

CORRESPENDENCE ADDOCT PAIK ROAD
TITLE ADDOCT PAIK
STREET: 100 Abbott PAIK ROAD
COMPONER: LIB COMPATIBLE
COUNTRY: USA
APPLICATION DATA:
MEDIDM TYPE: Diskette
COMPONER: LIB COMPATIBLE
COMPONER: LIB COMPATIBLE
COMPONER: LIB COMPATIBLE
COMPONER: LIB COMPANER: DOSSETTION DATA:
APPLICATION DATA:
PRICK APPLICATION DATE:
FILING DATE:
RIGHER APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATE:
RIGHER APPLICATION DATA:
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APPLICATION DATA:
APPLICANTION D
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us-09-099-823-3.rnpb

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61 GGGTAGGTCCAGGTGCTCCGGGCTCTGTGTGTGGGTAGGGTGGGCTCTGGAGGTGCAG 120
                                                 121 ACCCGGGGCTGCCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAAATGT 180
                                                                            181 CCTCCTCCGAGAGTCCCTTGCGCTGCACTTTCTTAAATTCTTCCAGGGCCTCCCGGT 240
                                                                                                                                                                                                                                                                  141 TGGTATCAGAATTCCTACCCACAAGCTTTCCCATGTGGAGCAGCAGGCCCCCATGTGCTGGT 300
                                                                                                                                            181 CCTCCTCCGAGAGTCCCTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGT 240
                                                                                                                                                                                                                                         241 TGGTATCAGAATTCCTACCCACAAGCTTTCCCATGTGGAGCAGGCCCCCCATGGTGCTGGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: REATOCHVIL, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: SCHERFEL, CHRISTI
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: YOUNGE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: POR DETECTING DISBASES OF THE BREAST
WUNDER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                 301 CITTGCAGTAAAGATGTAGTGGTCCCTCCTGGGCAG 337
                                                                                                                                                                                                                                                                                                                                                            301 CTTTGCAGTAAAAGATGTAGTGGTCCCTCCTGGGCAG 337
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COMPUTER: IMA COMPATIBLE
COMPUTER: IMA COMPATIBLE
CONFUTER: IMA COMPATIBLE
CONFUTER: FASTEN
CONFUTERING NOT NICONS
APPLICATION NUMBER: US/09/099,823
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COHEN, MAURICE
COLFITTS, TRACEY L.
PRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUABER:
FILING DATE: 20-UNN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Abbott Laboratories: 100 Abbott Park Road Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/09099823
; Patent No. US20020018990A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441 REFERENCE/DOCKET NUMBER: 612 TELECOMMUNICATION INFORMATION: 1ELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 847/938-2623
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ADDRESSEE: Abbott La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: 1
APPLICANT: 0
APPLICANT: 0
APPLICANT: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-099-823-4/C
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APPLICANT:
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Sequence 803, Application US/09833381
Befort No. US20020133090A1
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
APPLICANT: Robison, No. US20020132090A1e1 Nucleic Acid and Protein Homologs
FILLS TRYERION: NO. US200201333381
CURRENT PRILIKO NUMBER: 2000-104-11
PRIOR PILIKO DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2020
SEGTWARE: PastSEQ for Windows Version 3.0
SEQ ID NOS: 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CCTCCTCCGAGAGTCCCTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CCICCICCGAGAGICCCIIGCGCIGCACCAAIIICIIAAAIICIITCAGGGCCICCCGGI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 IGGIATCAGAATTCCTACCCACAAGCTTTCCCATGTGGAGCAGCACCCCATGGTGCTGGT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGGGAGAAGGACTTTATTTGGAGTCAGGTGGGTGGGAGCAGGGAAGGGTCATGGCTGGA 60
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                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 337; DB 10; Length 337; Best Local Similarity 100.0%; Pred. No. 9.8e-90; Matches 37, Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 337; DB 10; Length 501; 100.0%; Pred. No. 1.1e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.Pl
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                     LENGTH: 337 base pairs;
TYPE: nucleic acid
STRANDDNESS: single
TOPOLOGY: linear
US-09-099-823-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.03
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-833-381-803
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137 GIGITCGGGAACGCAGCITCCCGTCTGCAGGGGCGTGAAAAIGICCTCCTCCGAGAGTCC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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US-09-911-845-1/C
US-09-911-845-1/C
Sequence 1. Application US/09951845
Sequence 1. Application US/09951845
Sequence 1. Application US/09951845
SEQUENCE 1. Sequence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 337; DB 10;
100.0%; Pred. No. 1.3e-89;
ive 0; Mismatches 0;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPAX: 847/938-2623
35,441
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CRRACATENSTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDENESS: single
'TOPOLOGY: linear
US-09-099-823-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 337; Conservative
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    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
TOCATION: (8)...(517)
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US-09-951-845-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TGGTAICAGAATICCIACCCACAAGCITICCCAIGIGGAGCAGGCCCCCAIGGIGGIGGI 300
                                                                                                                                                                                                                                                                                    121 ACCCGGGGGCTGCCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAAATGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 CCICCICCGGAGGGCCCTGCGCTGCACTATTCTTAATTCTTCAGGGCCTCCCGGT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                 1 GGGGGAAAGAACITIATITIGAACICAGGIGGGIGGGAAGCAGGGAAGGGICAIGGCIGGA 60
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APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HONGES, STEVEN C.
APPLICANT: KRANCGNILL, JON D.
APPLICANT: KRANCGNILL, JON D.
APPLICANT: REARCHILL, JON D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: TU, HONG
APPLICANT: APPLICANT: APPLICATE TO APPLICATE TO APPLICANT: APPLICANT:
                                                                                    Query Match 100.0%; Score 337; DB 10; Length 692; Best Local Similarity 100.0%; Pred. No. 1.3e-89; Matches 337; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 CTTTGCAGTAAAAGATGTAGTGGTCCCTCCTGGGCAG 337
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OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/099,823
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION BATA: 8/879,354
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BILLING-MEDEL, PATRICIA APPLICANT: COHEN, MAURICE APPLICANT: COLPITS, TRACEY L. APPLICANT: FRIEDRAN, PAULA N. APPLICANT: GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09099823
Patent No. US20020018990A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Diskette
IBM Compatible
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Abbott
STREET: 100 Abbot
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-099-823-5/c
                                 US-09-099-823-4
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516 TCCTGGAGAGCAGGTTTCGCTCTGCGCGAGTTCCAAAATCTCCTGGTTC---AATCCTTT 460

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RESULT 8
US-10-143-576-1/c
is Sequence 1, Application US/10143576
sequence 1, Application No. US20030013151a1
sequence 1 INVENTION: USES THEROF
string OF INVENTION: USES THEROF
string OF INVENTION: USES THEROF
string OF INVENTION: USES THEROF
string NAMER: PLILING DATE: 2002-05-13
sopropras: EastSEQ for Windows Version 4.0
ssq 1D No. 1
seq 1D No. 1
seq 1D No. 1
seq 1D No. 1
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WILLIAN: Brian
APPLICANT: TUTNET:
APPLICANT: TUTNET:
TITLE OF INVENTION: No. US20020107375Alel Human Lipocalin Homologs and Polynucleot
TITLE OF INVENTION: No. US20020107375Alel Human Lipocalin Homologs and Polynucleot
TITLE OF INVENTION: No. US2004047
CURRENT APPLICATION NUMBER: US 60/203,874
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 GIATCAGAATTCCTACCCACAAGCTTTCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 TCCTCCGAGAGTCCCTTGCGCTGCAATTTCTTAAATTCTTCCAGGGCCTCCCGGTTG 242
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  200 GCGCIGCACCAATITCITAAATICITCCAGGGCCICCCGGTTGGTATCAGAATICCIACC 259
                                                                                        260 CACAAGCTTTCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAAAGATGTA 319
                                          459 GGCTCTTGAGAATTCCCGAAAATCCTCCAAGGCCTCTGGCTCTGGCTCTGGATCCCTTCC 400
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                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/09854847 Patent No. US20020107375A1
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                                                                                                                                                                                        320 GTGGTCCCTCCTGGG 334
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; ORGANISM: homo sapiens
US-09-854-847-25
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                                                                                     ACCCACAAGCTTTCCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAAGAT 316
197 CTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGTTGGTATCAGAATTCCT 256
                                                                                                               3;
                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09374671

Sequence 1, Application US/09374671

Patent No. US20020012963A1

GENERAL INFORMATION:
APPLICANT: Manieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog TITLE OF INVENTION: Dander and Uses Therefor NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORING TAGE THORNATION:
NAME: Mandragours, Amy E.
REGISTRATION UNGER: 56,207
REFERENCE, DOCKET NUMBER: 1MI-026CP (IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 525 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDED ADDRESSES.

ADDRESSES: LAHIVE & CORFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: (02109
COMPTRY: USA
ZIP: (02109
COMPUTER: FLOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
PRELIGATION NUMBER: US/09/374,671
FLING DATE:
CHASCITCATION NUMBER: US/09/374,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,861
                                                                                                                                                                                i. 525 base pairs
nucleic acid
DEDNESS: single
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TOPOLOGY: lin
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LOCATION:
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US-09-374-671-1
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US-09-374-671-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.2%; Score 44.6; DB 10; Best Local Similarity 51.8%; Pred. No. 0.00063; Matches 101; Conservative 0; Mismatches 94;
TITLE OF INVENTION: 32 Human secreted proteins File REFERENCE: P2044P1
                                                                             FILE KREEKUNC: FLOWER: US/09/800,729
CURRENT APPLICATION WIMER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION WIMER: PCT/US/00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR PILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
SUGWARE: PALENTIN VOS: 217
SOFWARE: PALENTIN VET. 2.0
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Best Local Similarity 51.8
Matches 101; Conservative
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ORGANISM: homo sapiens
US-09-854-847-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-800-729-37
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105-09-564-847-1/C
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                                                                                                                                                                                        Query Match 13.2%; Score 44.6; DB 9; Length 555; Best Local Similarity 51.8%; Pred. No. 0.00062; Matches 101; Conservative 0; Mismatches 94; Indels (
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Best Local Similarity 51.8%; Pred. No. 0.00062;
Matches 101; Conservative 0; Mismatches 94;
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2:09-800-729-37/c
5:Sequence 37, Application US/09800729
; Patent No. US20020068319A1
; PERFAIL INFORMATION:
; APPLICARY: NI et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 TTGCAGTAAAAGATG 317
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CORGANISM: homo sapiens
US-09-854-847-1
                                                                                                           Homo sapiens
                                                                                                      ; ORGANISM: Ho
US-10-143-576-1
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PRIOR PELICATION NUMBER: 60/049911
PRIOR PLIING DATE: 1997-06-18
PRIOR PELICATION NUMBER: 60/05974
PRIOR PELICATION NUMBER: 60/05913
PRIOR PLIING DATE: 1997-06-16
PRIOR PELICATION NUMBER: 60/05913
PRIOR PLIING DATE: 1997-09-17
PRIOR PLIING DATE: 1997-09-18
PRIOR PLIING DATE: 1997-09-19
PRIOR PLIING DATE: 1997-10-17
PRIOR PLIING DATE: 1997-10-17
PRIOR PLIING DATE: 1997-10-17
PRIOR PLIING DATE: 1997-10-24
PRIOR PLIING DATE: 1997-10-27
PRIOR PLIING DATE: 1997-10-29
PRIOR PLIING DATE: 1997-11-27
PRIOR PLIING DATE: 1997-11-27
PRIOR PLIING DATE: 1997-11-17
PRIOR PLIING DATE: 
                                                                                                                                                                                        Sequence 17, Application US/09854847

Patent No. US20020107375A1

GENERAL INFORMATION:

APPLICANT: MITCH.

APPLICANT: TURNEY. C. ALGRANDER UT.

TITLE OF INVENTION: No. US20020107375A1e1 Human Lipocalin Homologs and Polynucleotide PILE REFERENCE: LEX-0173-USA.

CURRENT PELLNO DAITE: 2001-09-10.

PRIOR FILING DAITE: 2000-05-12.

NUMBER OF SEQ. ID NOS: 28

SEQ. ID NOS: 28

SEQ. ID NOS: 28

SEQ. ID NO 17.

LENGTH: 597
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Best Local Similarity 51.8%; Preel No. 000604;
Maktches 101; Conservative 0; Mismatches 94; Indels 0; Gaps
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TITLE OP INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
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Sequence 237, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gao, Wei-Qiang
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Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L.
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                                                                398 TAGATGTAAAGGACG 384
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CORGANISM: homo sapiens
US-09-854-847-17
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APPLICANT:
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PRICR APPLICATION NUMBER: 60/069212
PRICR RILLING DATE: 1997-12-11
PRICR APPLICATION NUMBER: 60/069278
PRICR PILLING DATE: 1997-12-11
PRICR APPLICATION NUMBER: 60/06934
PRICR PILLING DATE: 1997-12-11
PRICR PILLING DATE: 1997-12-11
PRICR PILLING DATE: 1997-12-16
PRICR PILLING DATE: 1998-01-23
PRICR PILLING DATE: 1998-01-29
PRICR PILLING DATE: 1998-01-29
PRICR PILLING DATE: 1998-01-29
PRICR APPLICATION NUMBER: 60/073612
PRICR APPLICATION NUMBER: 60/073612
PRICR APPLICATION NUMBER: 60/073612
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PRICR APPLICATION NUMBER: 60/074066
PRICR APPLICATION NUMBER: 60/074092
PRICR APPLICATION NUMBER: 60/077091
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PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/083345
PRIOR PILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-04-14
APPLICATION NUMBER: 60/061817
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/077791
THE 1998-03-12
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APPLICATION NUMBER: 60/079663
APPLICATION NUMBER: 1998-02-27
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FILING DATE: 1998-02-27
APPLICATION NUMBER: 60/079728
APPLICATION NUMBER: 1998-03-27
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/084637
FILING DATE: 1998-05-07
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PRIOR PAPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
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APPLICATION NUMBER: 60/080165
FILING DATE: 1998-03-31
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FILING DATE: 1998-04-14
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
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PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
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123 CCGGGGGGCTGCCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAATGTCC 182
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51.3%; Pred. No. 0.0021;
tive 0; Mismatches 95; Indels
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741
PRIOR PLICATION NUMBER: 60/088741
PRIOR FILING DATE: 1998-06-10
PRIOR PLICATION NUMBER: 60/088810
PRIOR PLILOR DATE: 1998-06-11
PRIOR PLILOR DATE: 1998-06-11
PRIOR PLILOR DATE: 1998-06-17
PRIOR PLILOR DATE: 1998-06-17
PRIOR PLILOR DATE: 1998-06-17
PRIOR PLILOR DATE: 1998-06-17
PRIOR PLILOR DATE: 1998-06-18
PRIOR PLILOR DATE: 1998-06-18
PRIOR PLILOR DATE: 1998-06-19
PRIOR PLILOR DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090349
PRIOR PLILOR DATE: 1998-06-24
PRIOR PLILOR DATE: 1998-06-26
PRIOR PLILOR DATE: 1998-06-26
PRIOR PLILOR DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PLILOR DATE: 1998-06-26
PRIOR PLILOR DATE: 1998-06-26
PRIOR PLILOR DATE: 1998-06-26
PRIOR PLILOR DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09180
PRIOR PLILOR DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09180
PRIOR PLILOR DATE: 1998-07-07
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25-10-121-049-237/c
; Sequence 237, Application US/10121049
; Publication No. 05200300223981
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary B.
Goddard, Audrey
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0; Mismatches 95; Indels

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123 CCGGGGGCCTGCCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAATGTCC 182
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  Matches 100; Conservative
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                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DAME: 2002-04-12
PRIOR APPLICATION TEMPOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
ENGINE OF SEQ ID NOS: 550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 762
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                                                                                                                                                                                                                                                                                                                                      Ouery Match 12.8%; Score 43; DB 9; Length 762; Best Local Similarity 51.3%; Pred. 80. 0.0021; Matches 100; Conservative 0; Mismatches 95; Indels
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US-10-123-904-237/C

Sequence 237, Application US/10123904

Publication No. US2003002328A1

CENERAL INFORMATON:

APPLICANT: BAREALKEVID P.

APPLICANT: BAREALM.
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Goddard, Audrey
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Gurney, Austin L.
Sherwood, Steven
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APPLICANT: Wood, William
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                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-237
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; ORGANISM: Homo Sapien
US-10-123-904-237
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183 TCCTCCGAGAGTCCCTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCCGGTTG 242
                                                                                          579 CAGGGCGCCTCCTTGCTCTCAGGGTTGCATGCATCTGACTGGGGCAGCATGACCATCATG 520
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399 TAGATGTAAAGGACG 385
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RESULT 1
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                                                             February 9, 2003, 22:05:30; Search time 936.771 Seconds (without alignments) 5826.269 Million cell updates/sec
                                                                                                                     1 GGGGGAGAAGGACTTTATTT.....TAGTGGTCCCTCCTGGGCAG 337
       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                   16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
                                                                                                                                       Scoring table: IDENTITY_NUC Gapext 1.0
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em_gss_hum:*
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AQ721811 AQ748616 CNSOOJTL CNSO156Q CNSO3NP3 CNSO3NP3

41 40.8 40.8 40.8 40.8 60.04 60.6

A1219510 qh24d02.x AA936288 on75f11.s AW049121 UT-W-BHI BB028765 BB028765 BB618259 BB618259 AW920286 ESF351590 AR877465 ud10d09.r AR877465 ud10d09.r AR871021 EST193789 BF288401 EST455992 R47029 Y358 Rat in AL258805 Tetracocon BF35894 UT-R-CA1-BF405890 UT-R-CA1-BF405890 UT-R-CA1-BF405890 UT-R-CA1-BF40589 UT-R-CA1-BF40589 UT-R-CA1-BF40589 UT-R-CA1-BF40585 UT-R-CA1-AL05659 DT-R-AJO-AL072271 Drosophil AL6565 UT-R-BHO-AL6565 UT-R-BHO-AL6565 UT-R-CA1-BF40565 UT-R-CA1-AL072271 Drosophil AL656592 602274517 BF505334 60315481 BF52536 603274517 BF52596 603274517 BF32596 60317477 AL67668 Drosophil AL25336 Tetracodon ALA10768 Drosophil AL25336 Tetracodon ALA10779 Tetracodon

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9 AA460323 9 AI251747 9 AA460385 10 AW513637 9 AA977608 9 AI143970

337 415 532 513 349

100.0 99.5 99.4 99.1

335.4 335.4 335 335 333.8 328.8

Score

Result

Description

160323	
SOC	AA460323 337 bp mRNA linear EST 09-JUN-1997
NOITINI	zx51e06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795778
	3' similar to TR:G207551 G207551 ODORANT-BINDING PROTEIN. ;, mRNA
	sequence.
ESSION	AA460323
RSION	AA460323.1 G1:2185139
WORDS	EST.
JRCE	human.
RGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
FERENCE	1 (bases 1 to 337)
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
	Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.
	, Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie
	T., Waterston, R. and Wilson, R.
LITTE	WashU-Merck EST Project 1997
TOURNAL	Unpublished (1997)
DMENT	Contact: Wilson RK
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: est@watson.wustl.edu
	This clone is available royalty-free through LLNL ; contact the
	IMAGE Consortium (info@image.llnl.gov) for further information.
	Possible reversed clone: similarity on wrong strand

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/idb.losu="u
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1 (bases 1 to
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco. High quality sequence stop: 396.
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                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lmAGE:1854287"
/clone=lib="Soares_NFL_T_GBC_SI"
/lab_host="DH10B"
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477 bp mRNA linear EST 05-NOV-1998
qh90f12.x1 Scares_NFL_T_GBC_£1 Homo sapiens cDNA clone
IMAGE: 1854287 3' similar to TR:Q63613 Q63613 ODORANT-BINDING
PROFEIN ', mRNA sequence.
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1 (bases 1 to 477)

NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCT-CGAP ittp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
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/clone_lih="Soares_testis_NHT"
/sex="male"
                               Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 323.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CTTTGCAGTAAAAGATGTAGTGGTCCCTCCTGGGCAG 337
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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Best Local Similarity 100.0
Matches 337; Conservative
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                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 532) NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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/clone=lib="NCI_CGAP_UTI"
/clone_lib="NCI_CGAP_UTI"
/closue_type="Well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
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99.4%; Pred. No. 3.8e-80;
tive 0; Mismatches 2;
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Best Local Similarity 99.49
Matches 335; Conservative
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          Washu-Werck EST Project 1997

Unpublished (1997)

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Fax: 314 286 1800
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Fax: 314 286 1800
Fax: 314 286 1810
Fax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:795778"
/clone_lib="Soares_testis_NHT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 415
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/lab_host="DH10B"
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AUTHORS TITLE

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                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (basea to 549)
NGT-CGAP http://www.nobi.nlm.nih.gov/noicgap.
NGT-CGAP intsitute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                              sequence.
AI143970
AI143970.1 GI:3665779
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                                                                                                                                                                   Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Butaryota; Metazoa; Chordata; Catarrinii; Hominidae; Homo.

12 (bases 1 to 513)

RS NII-CGAP HILP://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Ornablished (1997)

AL Ornablished (1997)

Instit capps-r@mail.nih.gov
This clone is available royalty-free through LIML; contact the
This clone is available royalty-free through LIML; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 77 Std Error: 0.00
Seq primer: -40ml3 Fwd. Er from Amersham
High quality sequence stop: 339.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GGGGGAGAAGGACTTTATTTGGAGTCAGGTGGGAGGAGGAAGGGAAGGTCATGGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 513
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                        PROTEIN. ;, mRNA sequence.
AA977608
AA977608.1 GI:3155054
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RESULT 6 AI143970

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/law_lubs__unubded; Vector: pTyT3D-Pac (Pharmacia) with /note_"Organ: pooled; Vector: pTyT3D-Pac (Pharmacia) with amodified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from thee normalized libraries (fetal lung NbHiJ9W, testis NHT, and B-Cell libraries (fetal lung NbHiJ9W, testis NHT, and B-Cell libraries (fetal lung NbHiJ9W, testis NHT, and B-Cell libraries are mixed, and ss circles were maded in vit.cGAP_GCB1) were mixed; from pools of collowing as ECR-amplified oDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 78648-728711, am 7729965-731399, subtraction by Bento Soares and M. Patima Bonaldo. 1 others
                                                                                                                                 431 bp mRNA linear EST 29-APR-1998 on75fil.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone PAGES-1562541 3' similar to TR:063613 Q63613 ODORANT-BINDING PROTEIN: ', mRNA sequence. AA936288 BSS 88 GI:33094206 EST.
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarxhini; Hominidae; Homo.
I (base 11 to 431)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP close Institute, Cancer Genome Anatomy Project (CGAP),
Mational Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Context: Schert Strausberg, Ph.D.
Context: Robert Strausberg, Ph.D.
Email: cappb:-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact information.
IMAGE CONSORTHUM (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 344.

1. 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .431
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Tumor Gene Index
Unpublished (1997)
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//D_xref="raxon:1606"
//D_xref="raxon:1606"
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//Lone="Inbac=184500"
//Lone="Inbac="Data"
//Lone="Torgan: pooled" | Vector: pr773D-Pac (Pharmacia) | Vichote="Organ: pooled" | Vector: pr773D-Pac (Pharmacia) | Vichote="Organ: pooled" | Vector: pr773D-Pac (Pharmacia) | Vichote="Organ: pooled" | Vector: pr18742 
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Bukaryota; Metazoa; Chordatas; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
MCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
MRI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
MRI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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   318 CTTTGCAGTAAAAGATGTAGTGGTCCCTCCTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'umor Gene Index
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                                                                                                                                                                                DEFINITION
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AUTHORS
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Mon Feb 10 11:11:55 2003

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Lusson T. Carnidl.P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramcho,K., Hori,F., Ishi,I.Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Murametsu,M. and Hayashizaki,Y. Takeda,Y., Takeda,Y., Takeda,Y., Tayaki,Y., Suzuki,H., Murametsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB028765 BIKEN full-length enriched, 6 days neonate head Mus musculus cDNA clone 5430417003 3', mRNA sequence.
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Konno,H., Pukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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URL;http://genome.gsc.riken.go.jp,
URL;http://genome.gsc.riken.go.jp,
URL;http://genome.gsc.riken.go.jp/
Carninci.P., Shipata.Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramateu,M. and Bayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNss to
prepare full-length cDNR ibraries for rapid discovery of new
genes. Genome Resc. in (10), 1617-1650 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B.,
Watahi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jun 8, 2000 this sequence version replaced gi:8383516.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                                                                                                                                                                                                                                                                                                                                            59 GAGGGTAGGTCCAGGTCCCGGCCTCTGTCTGGTGGTAGGGTGGGCTCTGGAGGTGC 118
                                                                                                                                             107 caddrorgergaagggargroccagcrrgergrregaagcaagcregcrcagcrgrreg 166
                                                                                                                                                                                                        . 119 AGACCCGGG-GGCTGCCTAGTGTTCGGGAACGCAGCTTCCCCGTCTGCAGGGGGGGTGAAAA 177
                                                                                                                                                                                                                                                               167 AGACCTGGGTAGCTGCCTAGTCACTTTCAACATTTATCTCCGGATCTCTGGCACAAACA 226
                                                                                                                                                                                                                                                                                                                             178 TGTCCTCCTCCGAGAGTCCCTTGCGCTGCACCAATTTCTTAAATTCTTCCAGGGCCTCCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 GGTIGGIATCAGAATICCIACCCACAAGCTITCCCAIGIGGA---GCAGGCCCCCAIGGI 294
                               4; Gaps
60.4%; Pred. No. 5.2e-11;
live 0; Mismatches 105; Indels
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BB028765.2 GI:16258092
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   Best Local Similarity 60.4
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                 AW049121
UT-M-BHI-amt-h-10-0-UI-31 WHE BMAP_M_S2 Mus musculus cDNA clone
UI-W-BHI-amt-h-10-0-UI 3', MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 501)
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Normalization and subtraction: two approaches to facilitate gene
   144 FGGTATTAGGATTCCTACCACACAGCTTTCCCATGTAGGGGCCCCCACGGCGCGCTGGT 302
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                                                                                             301 CITIGCAGTAAAAATGTGTGGTCCCTCCTGGGCAG 337
                                                                                                                               303 CTTTGCAGTAAAAGACGTA-TGTNCCGTCCCGGGCAG 338
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TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=olfactory-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mEST@mail.nih.gov
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Fax: 301 443 9890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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Source

FEATURES

discovery

AUTHORS TITLE JOURNAL MEDLINE

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VERSION KEYWORDS

ORGANISM

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RESULT 9 AW049121

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EST 26-0CT-2001
                 linear
                  mRNA
                  603 bp
                  BB618259
RESULT 11
BB618259/c
LOCUS
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Enkaryota Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Arakawar, C., Graninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, T., Okido, T., Salto, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Takeda, T., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, P., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse Egrs (Arakaya, P., et al. 2001)
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Context: Yoshihide Hayashisaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yoshama Institute
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*Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-Dased methods for the mouse full-length CDNA congular-lane sequence clustering for construction of a noredundant CDNA library. Genome Res. 11 (2), 281-289 (2001) and the construction of a construction of a construction of a noredundant CDNA library. Genome Res. 11 (2), 281-289 (2001) (X., Fukuda,S., Shingawa,A., Saitoh, T., Kayashi, Y., Ananaka,I., Alzawa K., Fukuda,S., Hara,A., Itoh,M., Kayashi,J., Shibata,K. and Hayashizaki,Y.
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GACAGAGAGAGAGCATCATATTTTTTTTTTTTTVN 3'], cDNA was
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BB618259 RIKEN full-length enriched, 6 days neonate head Mus
musculus cDNA clone 5430417003 5', mRNA sequence.
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5430417003"
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                                      Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                    CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with Euman Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/strain="C57BL/6J"
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/clone="5430417003"
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Location/Qualifiers
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                                                                                                                   ,K., Fukuda,S.
Hayashizaki,Y
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182 a

BASE COUNT

Query Match Best Local

δĀ d δŏ g δŽ g ŏ 셤 δ 셤 ö

Mon Feb 10 11:11:55 2003

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/note="Organ: uterus; Vector: pT773D-Pac (Pharmacia) with note="Organ: uterus; Vector: pT773D-Pac (Pharmacia) with pregnant mouse uterus, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

112 c 142 g 116 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1877465 S19 bp mRNA linear EST 21-JUL-1999 ud10609.rl Scares_NMPu Mus musculus cDNA clone IMAGE:1434737 5' similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 519)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Consortium (info@image.llnl.gov) for further information.
MGI:918805
                                                                                                                                                                            195 CCCTTGCGCTGCACCAALTTCTTAAATTCTTCCAGGGCCTCCCGGTTGGTATCAGAATTC 254
                                                                                                                                                                                                                                                         255 CTACCCACAAGCTTTCCCATGTGGAGCAGGCCCCCATGGTGCTGGTCTTTGCAGTAAAAG 314
                                                                                                                                                                                                                                                                                                                                      135 TAGTGTTCGGGAACGCAGCTTCCCGTCTGCAGGGGCGTGAAAATGTCCTCCTCCGAGAGT 194
                                                                                                                 ;
0
                                                                          Length 594;
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                                                                             score 70.4; DB 10; Length
Pred. No. 1.1e-08;
0; Mismatches 76; Indels
Xhol; Estimated insert size approx.1 kb"
169 a 153 c 148 g 124 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. :519
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="TRAGE:1434/37"
/clone_lib="Soares_NMPu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector to vector length is
seq primer: "SBMB1 rev2 ET from
High quality sequence stop: 503.
Location/Qualifiers
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/dev_stage="adult"
/lab_host="DH10B"
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AI877465.1 GI:5551514
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Best Local Similarity 60.4%;
Matches 116; Conservative
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A1877465/c
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I (bases 1 to 594).

I (bases 1 to 594).

I Lee, N. H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,

Kerlaryge, A.R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index

L Unpublished (1998)

Contact: Lee, NH

The Institute for Genomic Research

771, Medical Center Drive, Rockville, MD 20850, USA

772, Medical Center Drive, Rockville, MD 20850, USA

Fax: (301)-838-9208

Fax: (301)-838-9208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     594 bp mRNA linear EST 25-MAY-2000 EST31590 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIGT45 5' end, mRNA sequence. AM920286 AM920286.1 GI:8086095 EST.
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liver, embryo, heart, muscle, spleen"
/lab_host="SolR"
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Rattus norvegicus
Bukaryota: Metascos; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Rat gene index, normalized rat, norvegicus,
                                                                                                                                                                                                                                                                                                                                               107 CTCTGGAGGTGCAGACCCGGG-GGCTGCCTAGTGTTCGGGAACGCAGCTTCCCGTCTGCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                            166 GGGGCGIGAAAAIGICCICCICCGAGAGICCCIIGCGCIGCACCAAITICIIAAAITICII 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 CIGGCACAAACATGITITCCAGTCGGAGATTCATGGGCTTTATGAAATTCTTAAATTCTT 484
                                                                                                                                                                                                                                                                                                                                                                              226 CCAGGGCCTCCCGGTTGGTATCCAAATTCCTACCCACAAGCTTTCCCATGTGGA---GCA 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: "hise@tigr.org
This clone is available through the ATCC, contact the ATCC
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: MI3 Reverse.
Location/Qualifiers
1. .594
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                    21.5%; Score 72.6; DB 10; Length 603; 63.4%; Pred. No. 2.9e-09; tive 0; Mismatches 79; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 GGCCCCCATGGTGCTGGTCTTTGCAGTAAAAGATGTAGTGGTCCCTC 329
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/clone="RGIGT45"
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.44
Matches 144; Conservative
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Ration (1998) 1 to 322)

S Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pertea, G., Cho, J., Lee, Y., Raramycheva, S., Parvizi, B., Pertea, G., Sultana, R., Tasi, J., White, J., Quackenbush, J. and Lee, N. H. Sultana, R. Tasi, J., White, J., Quackenbush, J. and Lee, N. H. Sultana, R. Tasi, J., White, J., Quackenbush, J. and Lee, N. Ton Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
This (301)-838-3529
Fax: (301)-838-3529
Fax: (301)-838-3529
Fax: (301)-838-5200
Fax: (190)-835-2700 for further information.

Location/Qualifiers ö RSP BF288401 322 bp mRNA linear EST 28-NOV-2000 EST452992 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIGT39 3' sequence, mRNA sequence. Norway rat. Ratius ovregicus Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordatia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; /tissue_trpe="mixed tissue"
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/lab.ost="DR5-alpha"
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combination of ROV, RBR, RKI, RLI, RPL, RLW, RMU,
RRW, RPC, RPN"
1 67 c 99 g 71 t 149 GCAGCTICCCGICIGCAGGGGCGIGAAATGICCICCICCGAGAGICCCTIGCGCTGCAC 208 0; Gaps Organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="Raftg139"
/clone_lib="Rat Gene Index, normalized rat, Rattus norvegicus cDNA" Query Match 15.1%; Score 51; DB 12; Length 322; Best Local Similarity 61.8%; Pred. No. 0.0018; Matches 81; Conservative 0; Mismatches 50; Indels completed: February 10, 2003, 04:58:18 ne : 947.771 secs BF288401 BF288401.1 GI:11219471

Mon Feb 10 11:11:55 2003

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

em_htg_vrt:*

em_htg_hum:* em_htg_inv:* em_htg_other:*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 648.8 648.8 589.8 573.8 573.8 560 560 February 9, 2003, 22:02:40 ; Search time 2254.33 Seconds
(Without alignments)
8933.518 Million cell updates/sec 1 GACGCCCAGTGACCTGCCGA.....ATAAAGTCCTTCTCCCCCCA 692 4109280 GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-09-099-823-4 692 gb_ba:* gb_htg:* gb_in:* GenEmbl:* Scoring table: Perfect score: Database : Searched: Sequence: Run on:

A/251024 Homo sapi.
A/251024 Homo sapi.
A/281340 Sequence
AX08346 Sequence
AX083548 Sequence
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AX251023 Homo sapi.
A76734 Rat odorant
B002756 Mus muscu
M06424 Human tear
AX251323 Sequence
X67647 H.sapiens m
AX214532 Sequence
X67647 H.sapiens m
XX214532 Sequence
X50416 R.norvegicu
X50416 R.norvegicu
X50416 R.norvegicu
X50417 Canis fam
AR070177 Canis fam AZ51025 Homo sapl AC002090 Genomic s AC002090 Genomic s AL72236 Human DNA AC00230 Homo sapi AL772161 Homo sapi AZ51029 Homo sapi AZ51029 Homo sapi AC00396 Genomic s AC01642 Human DNA AC01642 Human DNA AC01647 Homo sapi AX454620 Sequence AX491098 Sequence AX083544 Sequence AX251026 Homo sapi Sequence Homo sapi Sequence Sequence Description SUMMARIES RNVEGP2B RNVEGP DB % Query Match Length D 21.1 753 21.0 525 21.0 525 21.0 525 19.7 1359 19.7 36612 19.7 36612 19.7 210243 19.7 210243 19.5 10664 19.5 10

D38581 Mouse mRNA F319463 Macropus D38580 Mouse mRNA

MUSVNSPIIB

linear PAT 06-JUL-2002 human. Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Bominidae; Homo. Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. DNA AX454620 739 bp D Sequence 205 from Patent W00208284. AX454620 AX524620.1 GI:21713934 LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS RESULT 1

and Ye, W. JOHNSON, PRESENT, NO. 1010-1014, A. 2019, 31-JAN-2002. Generated, T. 00 1010-244, A. 2019, 31-JAN-2002. Andrey (19), 10-Cutol, 10-Cu	LOCUS AX491098 ACCESSION AX491098 VERSION AX491098.1 G1 KEYWORDS SURGE Numan. ORGANISM Homon sapiens CRGANISM Homon sapiens EUKATYOTA: Met Mammalia; Eutr REFERENCE BARET, K. P., FR AUTHORS GOGOWSK!, P.J., FR AUTHORS AND TOWN. TITLE COMPOSITIONS GLISCHELL: WO DIG	Genentech, Inc. Source 17 Source /orga BASE COUNT 210 a ORIGIN	Query Match Best Local Similarity Matches 690; Conservat QY GAGGCCAGTGACCTQ	61 61 121 121	Oy 181 CAGGARGGIFCCC Oy 241 TCACCTTCATGAGGG Oy 241 TCACCTTCATGAGGG Db 241 TCACCTTCATGAGGGG OO 301 AGCCTGGGAATARCA	301 361 361 421	421 421 481 541 541 601
	and Ye,W. Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis. Ascentiers involving anglogenesis. Ascentier, W. 0202284.A. 205 31-3AN-2002; Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Nap Genentech, Inc. (US); Baker, Kevin P. (US); Genber, Hanspeter (US); Gerber, Wary B. (US); Audrey (US); Gerber, Hanspeter (US); Gernitsen, Mary B. (US); Hanspeters, Soct A. (US); Paoni, Jann, Van Hilan, Kenneth J. (US); Stephan, Jean-Philippe F. (US); Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, I. (US) L. (US) Location/Qualifiers 1. (TS) Approximate—"Homo sapiens" Approximate "Homo sapiens" Approximate "Asson:9606" 210 a 207 c 205 g 117 t	Query Match 99.5%; Score 688.8; DB 6; Length 739; Best Local Similarity 99.7%; Pred. No. 7.2e-146; Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 1 GACGCCCAGTGACGAGGTCGGAAGACACAGAAGAATGAAGACCTGTTCC 60	I GACCECCAGIGACCIGACGAGGGGGGGGGGGGGGGGGGGG	181 CCAGGAAGGTGTCCCAGTGAAGGTGACCCCTGGGCGGTGGGAAGTTGGAAGCCAGGT 181 CCAGGAAGGTGCCCAGTGAAGGTGACCCCTGGGCGGTGGGAAGTTGGAAGCCAGGT 181 CCAGGAAGGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGC 241 CCACGTCATGAGGGAGGAGGCACCAGGAAGAAAATCCTGATGCGGAAGGGGGGG 241 TCACCTTCATGAGGGAGGAGGATGCATCCAGAAAAAATCCTGATGCGGAAGG	10 AGCCTGGCAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCA	421 GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAAT 421 GAAAGCTTGTGGGTAGGAATTCTTGATACCAACCGGGAGGCCTTGGAGAATTTAAGAAAT 421 GAAGCTGCGAGGGAATTCTGATACCAACCGGGAGCCTTGGAAGAATTTAAGAAAT 481 TGGTGCAACGGAAGGAATTCTGGAGGAACATTTTCACGCCCCTGCAACGAGGAAGCT 1	541 GCGTTCCCGAACACTAGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCCA

RESULT 2 AX491098

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PAT 16-AUG-2002
                                                                                                                 stazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
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200690-A 205 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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739 bp I
from Patent WO0200690.
                                                                                                                                                                                                                                                                                         rinc. (US)
cation/Qualifiers
.739
rganism="Homo sapiens"
b_xref="taxon:9606"
207 c 205 g 117
                                                 31:22323886
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Db 421 AAGCITOTGGGTAGGAATTCTGATACCAACCGGAGGCCCTGGAAGAATTTAAGAAATTG 480 QY 483 GTGCAGCGCAAGGGACTCTCGGAGGAGACATTTTCACGCCCCTGCAGACGGAAGCTGC 542	541 603 601	OY 663 CTGACTCCAAATAAG 678 Db 661 CTGACTCCAAATAAAG 676	×		ORGANISM HOMO Saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 676)		200 200 106	REFERENCE 2 (pases 1 to 6/6) AUTHORS Gachon,A.M. TITLE Direct Submission JOHNNAL Submitted (26-0CT-1999) Laboratoire de Biochimie Medicale - INSERM	U384, Uni Dunant, C		gene 43.:555 /gene="OBPIIb" CDS 43.:555 /dene="GRPIIb"	/codon_start=1 /product="putative odorant-binding protein b-a" /protein_id="3133.1" /db xref="G1:6900077"	/translation="MKTLFLGVTLGLAAALSFTLEEDITGTWYVKANYVDKDFPEDR RPRKYSPVKYPALGGGKLEATFPMEDBCIOKKILMRKTEEPGKKSAYGGRKLMYLQ :	160 a 200 c 204 g 112 t		OY 3 COCCLAGICACCTGCCAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCTGTTCCTG 62
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OY 661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCA 692	AX003344 AX083544 676 bp DNA linear PAI 28-FEB-2001 DEFINITION Sequence 9 from Patent W00112806. ACCESSION AX083544.1 GI:13185354 VERSION AX083544.1 GI:13185354 SOURCE human	NISM	TITLE Odorant-binding human proteins fixing hydrophobic ligands: polypeptides and polyneticities coding for said polypeptides and polyneticities and polyneticities and polyneticities and polyneticities and polyneticities and polyneticities and uses thereof parenties. Wo 0112806-A 9 22-FEB-2001; Universite d'Auvergne (FR); Pitiot, Gilles (FR)	ree 1676 /organism="Homo sapiens" /db.xref="taxon:9606" 43555		LGVTLGI	200 c 204 g 112 t	Query Match 97.7%; Score 676; DB 6; Length 676; Best Local Similarity 100.0%; Pred. No. 5.7e-143; Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AY 3 CGCCAGTGACCTGCCGAGGTCGGCAGCACCAGAGGTCTGGAGATGAAGACCTGTTCCTG 62	OY 63 GGTGTCACGCTCGCCTGGCCTGCTCCTTCACCCTGGAGGAGGAGATATCACA 122	OY 123 GGBACCTGGTBACGTGATGGTCGATBABGBACTTTCCGGAGGACGGCCC 182	DY 183 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCTGGGGCAGGTGGGAAGTTGGAAGCCACGTTC 242	QY 243 ACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGGGG 302	QY 303 CCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGG 362 Db 301 CCTGGCAAATACAGCGCCTATGGGGGCAGGAACTCATGTACCTGCAGGAGCTGCAGGG 360	363	423 AAGCTTGTGGGTAGGAATTCTGATACCAACGGGAGGCCCTGGAAGAATTTAGAAATTG

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Logescyler"
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HOMO sapilens mRNA for putative odorant biding protein aa (OBPIIa
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#0751031.1 GI:6900066
#0751031.1 GI:6900066

GBPIIA gene; odorant binding protein.

Homo sapiens.

BOMO sapiens

BUMARDOR; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 676)
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                                                                              Score 648.8; DB 6; Length 676; pred. No. 8.3e-137; 0; Mismatches 17; Indels 0.
                                              115 t
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                                                                               Query Match 93.8%;
Best Local Similarity 97.5%;
Matches 659; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
Priiot, G., Lacazette, E. and Gachon, F.
Odorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and
uses thereof
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Detent: WO 0112806-A 1 22-FEB-2001,
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 676
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122 c 217 g 123 f 12
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

(bases 1 to 725)
Pit.bot. G., Lacazette, B. and Gachon, F.
Codorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polymucleotides coding for said polypeptides and
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          543 GITCCCGAACACIAGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCCIACCACCAGAC 602
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/d. 483 . .483
/note="cDNA36 (725) /SM12 (hOBPIIa-beta)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Patent: WO 0112806-A 3 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
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Sequence 3 from Patent W00112806.
AX083538
AX083538.1 GI:13185348
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Matches 659; Conserv
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Lacazette, E., Gachon, A.M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from genomic duplicon at 9934 idfferential expression in the oral and genital spheres.
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                                                                                                              Hum. Mol. Genet. 9 (2), 289-301 (2000) 20076326
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/gene="OBPIIa"
/codon_start=1
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Aases 1 to 741)
                                                                                                                                                                                                                                                                                                                             GGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACA 553
                                                                                                                                                                                                        GGTGTCACGCTCGGCCTGGCCCTGCCCTCTCACCTTCACCTTGGAGGAGGAGGATATCACA 120
                                                                                                                                                                                                                                                              GGTGTCACGCTCGGCCTGGCCGCTGCCTTCCACCTTGGAGGAGGAGGAGGATATCACA 122
                                                                                                                                                                                                                                             GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAAGGAGGCCC 182
                                                                                                                                                                                                                                                                                                            183 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGAAGTTGGAAGCCACGTTC 242
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                                                      Score 589.8; DB 9; Length 725;
Pred. No. 2e-123;
0; Mismatches 17; Indels 49;
ELPGTDDIVFYCKDQRRGGLRYMGKLVGPCRCPHVGSPGHLTCR"
163 a 222 c 217 g 123 t
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Sequence 5 from Patent WO0112806.
AXO83540 AXO83540.1 GI:13185350
                                                         85.2%; & nilarity 90.9%; F Conservative 0;
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Best Local Similarity
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RPRKVSPVKVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lacazette, E., Gathon, A.M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and genital spheres.

Fun. Wol. Genet. 9 (2), 289-301 (2000)
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Direct Submission
Submitted (36-007-1999) Laboratoire de Biochimie Medicale - INSERM
Submitted (36-007-1999) Laboratoire de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
                                                                                                                                                                       301 CCTGGCAAATTCAGCGCCTATGGGGGCAGGAAGCTCATATACCTGCAGGAGCTGCCGGG 360
                              363 AGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGA 422
                                                  421 AAGCTTGTGGGGCCGTGCCGCTGTCCCCACGTCGGCTCACCTGGCCACCTCACCTGCAGG 480
                                                                                                                                                       TAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAA 493
                                                                                                                                                                                                                  GGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACA 553
                                                                                                                                                                                                                                                                                CTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGG 613
                                                                                                                                                                                                                                                                                                              601 CTAGGCAGCCCCGGGGTCTGCACCTCCAGAGCCCACCCTACCACAGACACAGAGCCCGG 660
                                                                                                                                                                                                                                                                                                                                             /product="putative odorant binding protein ab"
protein_id="CaB71319.1"
/db_xref="G1:6900069"
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AJ251022
AJ251022.1 GI:6900068
OBPIIa gene; odorant binding protein.
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/db_xref="taxon:9606"
/chromosome="9"
/map="9934"
/g. 483
/gene="OBPIIa"
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2 (bases 1 to 725)
Gachon, A.M.
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Homo sapiens
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661 CAGACACAGAGCCCGGACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCA 720
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88.9%; Pred. No. 8.3e-120;
ive 0; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9q34"
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/gene="OBPIIa"
                                 658 CCCACCTGACTCCAAATAAAG 678
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1 229 c
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//poted...j.de="CAC33324.1"
//boxeef="Galia185321"
//tansiation="MKTLEGVTIGIAAALSFTLEEEDITGTWYVRAMVVDKDFPEDR
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PWRALRAWGSTROBRRRYFSCPCRREARSWRTROPFGLAYGTLFFWR
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        Pitlot,G., Lacazette,E. and Gachon,F. odorant-binding human proteins fixing hydrophobic ligands: polypeptides and polypeptides and polypeptides and uses thereof
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88.9%; Pred. No. 8.3e-120;
Live 0; Mismatches 17; Indels 65; Gaps
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/codon_start=1
                                                          Patent: WO 0112806-A 5 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
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                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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www.manwcstrdsrriyscpcrreaarshyroppelhilospryhgygsphildles
HEA251024 1741 bp mENA linear PRI 02-FEB-2000 Homo sapiens mENA for putative odorant binding protein ag (OBFIIA
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AJ251024.1 GI:6900072

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Homo sapiens.

Homo docant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
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2 (Abases 1 to 741)
3 (Abases 1 to 741)
Direct Submission
Submitted (26-0CT-1999) Laboratoire de Biochimie Medicale - INSERM U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
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AJ251027.1 GI:6900078
AJ251027.1 GI:6900078
GBFIDs gene; odorant binding protein.
Homo sapiens.
Binaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthelia; Prinates; Catarrhini; Hominidae; Homo.
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Query Match 80.9%; Score 560; DB 6; Length 782; Best Local Similarity 86.4%; Pred. No. 1.1e-116; Matches 676; Conservative 0; Mismatches 0; Indels 106;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 782)
S Pitiot, G., Lacazette, and Gachon, F.
Odorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and uses thereof.

L Patent: WO 0112806-A 11 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)

I coation/Qualifiers
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/protein_id="Cac3337.1"
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                                                 181 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAACTTGGAAGCCACGTTC 240
                                243 ACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAG 302
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/db_xref="taxon:9606"
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/note="cDNA2098 (782) - forme longue (hOBPIIb-beta)"
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Sequence 11 from Patent W00112806.
AXO83546 AXO83546.1 GI:13185356
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PAT 20-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 CITITACIGCAAAGACCAGCACCAIGGGGGCCIGCICCACAIGGGAAAGCITGIGGGIAG 540
                                                                                497 ACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGGTTCCCGAACATA 556
                                                                                                  GGCAGCCCCGGGGTCTGCACCTCCAGAGCCCAACCTACCACCAGACACAGAGCCCGGACC 616
                                                                                                                                                         39 CIGGAGAIGAAGACCCIGITCCIGGGIGICACGCTCGGCCIGGCCGCTGTCCTTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 522;
                                                                                                                                                                                                                                                                                                                                                         linear
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Pred. No. 2.4e-106;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.

Unknown.

Unclassified.

Unclassified.

(I (bases 1 to 522)

Conkin, D.C.

Antibodies to lipocalin homologs

Antibodies to lipocalin homologs

Antibodies to lipocalin homologs

Incation/Qualifiers

1.522

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Sequence 1 from patent US 6365716.
AR204078
AR204078.1 GI:21500632
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ilarity 99.8%;
Conservative (
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Best Local Simi
Matches 515; (
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/protein_d="caB71324.1"
/bb_xref="61":690079"
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TPALMFALAIDFILKLIGTRRERIRWGQBAHVPAGAAQGGPLHILLQRPAPWGFAPH
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                                                                                                                                  Gachon, A.M.
Gachon, A.M.
Direct Submission
Submitted (18-00T-1999) Laboratoire de Biochimie Medicale - INSERM
Submitted (18-00T-1999) Laboratoire de Medecine, 28, place Henri
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
 l (bases 1 to 782)
Lacazette, E., Gachon, A. M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and genital spheres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 CTTTACTGCAAAGACCAGCACCATGGGGGCCTCCACACAGAAAGCTTGTGGGTAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AGGAAGGIGICCCCAGIGAAGGIGACAGCCCIGGGCGGGGGAAGIIGGAAGCCACGIIC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 ----ATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACTACAT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 ATTAGATGGGGGAGGAGGTCATGTACCTGCAGGAGCTGCCCAGGAGGACACTACAT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.9%; Score 560; DB 9; Length 782;
Best Local Similarity 86.4%; Pred. No. 1.1e-116;
Matches 676; Conservative 0; Mismatches 0; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 COCCCAGIGACCIGCCGAGGICGGCAGCACAGAGCTCIGGAGAIGAAGACCCIGIICCIG 62
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20076326
10607840
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                                                                                                                                                                                                                            1. .782
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/map="9934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 g
                                                                                                                                                                                                                                                                                                        /gene="OBPIIb"
43. .540
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/codon_start=1
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                                                                                                                          (bases 1 to 782)
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                REFERENCE
AUTHORS
TITLE
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                                                                                  JOURNAL
MEDLINE
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43. 300
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1 (bases 1 to 542)
Pitiot, G., Lacazette,E. and Gachon,F. odorant-binding human proteins fixing hydrophobic ligands: polypeptides and polynoleotides coding for said polypeptides and uses thereof
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                                                                           249 ATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGGC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 AAATACAGCGCCTATGGGGGGGAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGAAC 368
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362 CAIGGGGGCCTCCACAIGGGAAAGCIIGIGGGIAGGAAIICIGAIACCAACCGGGAG 421
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llarity 99.5%; Pred. No. 1.7e-86;
Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 0112806-A 13 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 542
//dryanism="Homo sapiens"
//db_xref=txxon:9606"
43. 300
                                                                                                                                               DNA
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Sequence 13 from Patent W00112806.
AXO83548
AXO83548.1 GI:13185358
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les 428; Conserv
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VERSION
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rprkyspykytalgggkleatftfwredrciokkilmktrebedkysayggrklwyld
elprdhyifyckdohhggllhwgklygrnsdynrealebfkklydrkglsedditp
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Eutheria, Primates, Catarihini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGCTC 338
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                                                                                            99 ACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAG 158
              361 CATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAG 420
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                                                             459 GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGAAGGGACTCTCGGAGGAGGACATTTTC
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Pred. No. 2.4e-106;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZymoGenetics, Inc. (US)
Location/Qualifiers
1. .523
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8. .>517
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                   ACCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 516
                                                                                                                                                             519 ACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 554
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Use of human phermone polypeptides
Patent: WO 0223201-A 1 21-MAR-2002;
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                                                                                                                                                                                                                                                                                                                       Sequence 1 from Patent W00223201.
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/db_xref="GI:21698380"
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Best Local Similarity 99.8%;
Matches 515; Conservative
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KEYWORDS
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BS124; breast; cancer; detection; diagnosis; prevention; treatment;
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human BS124 specific EST clone 1730294IH.
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AAX07453
AAH76463
AAS93598
AAQ69950
AAL03258
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 08-JUN-1999 (first entry)
(ABBO ) ABBOTT LAB.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Database :

New isolated BS124 polynucleotides and polypeptides - used for

WPI; 1999-105623/09.

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conditions
                         cancer; detection; diagnosis; prevention; treatment;
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 692; DB 20; Length 692; Best Local Similarity 100.0%; Pred. No. 4.2e-168; Matches 692; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a consensus BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                      New isolated BS124 polynucleotides and polypeptides - used detecting, diagnosing, preventing or treating diseases or of the breast, such as breast cancer
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consensus sequence
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 clone
                                                                                                                                                             98WO-US12862.
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Human BS124 specific EST
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                            BS124; breast; c
consensus; EST;
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   detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer
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0
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                                                                          The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                             Indels
                                                                                                                                                   Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;
                                                                                                                                                                             100.0%; Score 692; DB 20;
100.0%; Pred. No. 4.2e-168;
Live 0; Mismatches 0;
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                                                 Claim 11; Pages 94-95; 125pp; English.
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Best Local Similarity 100.0
Matches 692; Conservative
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                                                                                                                                                                                                                                                                               AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCA 360
                                                                                                                                                                                                                                                                                                                                                                                GGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGGCCTGCTCCACATGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 GAAAGCITGTGGGTAGGAAITCTGAIACCAACCGGGAGGCCCTGGAAGAATTTAAGAAAT 480
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61 IGGGTGICACGCTCGGCCTGCCCTGCCTTCACCCTGGAGGAGGAGGATATCA 120
                                                121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                 CCAGGAAGGIGICCCCCAGIGAAGGIGACAGCCCTGGGGCGGIGGGAAGIIGGAAGCCACGI 240
                                                                             DNA encoding protein of the invention #50.
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99US-0144758.
99US-0145698.
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99WO-US28551.
99WO-US30095.
2000WO-US00219.
2000WO-US00376.
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02-DEC-1999;
16-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosing, monitoring, staging, inaging and treating breast cancer (BC). The methods comprise measuring the levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelled and used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
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                                                                                     600
                                                                                                                  ACACAGAGCCCGGACCACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCC 660
                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast specific gene; breast specific marker; BSG; diagnosis; breast cancer; therapy; ss.
           541 GCGITCCCGAACACTAGGCAGCCCCCGGGTCTGCACTCCCAGAGCCCCACCTACCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human breast specific gene LS clone 1213903.
                                                                                                                                                                                                                                                                                        Example 1; Page 43; 45pp; English.
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99WO-US30095.
99WO-US30999.
99WO-US31274.
2000WO-US00219.
2000WO-US00277.
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20-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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02-JUN-1999;
23-JUN-1999;
20-JUL-1999;
26-JUL-1999;
28-JUL-1999;
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15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-OCT-1999;
30-NOV-1999;
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01-DEC-1999;
01-DEC-1999;
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                                                                                                                      AAC58615;
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                                                                    RESULT 5
AAC58615
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                                                                                                             Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene therapy -
                                   Fong S;
Hillan KJ;
                                                                                                                                                                                         The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                              61 IGGGTGTCACGCTCGGCCTGGCCGTGCCTGTCCTTCACCCTGGAGGAGGAGGAGATATCA 120
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                                                                                                                                                                                                                                                                                                                99.5%; Score 688.8; DB 22; Length 738; 99.7%; Pred. No. 2.8e-167; Live 0; Mismatches 2; Indels 0;
                                Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Pan J, Paoni NP, ROY MA, Smith V, Stewart TA, Tumas D; Watchabbe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                          Sequence 738 BP; 209 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                    Claim 2; Fig 99; 787pp; English.
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Best Local Similarity 99.7<sup>1</sup>
Matches 690; Conservative
           (GETH ) GENENTECH INC.
                                                                                           WPI; 2001-071395/08.
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Human PRO1283 protein UNQ653 encoding cDNA SEQ ID NO:169 BP. AAC58615 standard; cDNA; 739 (first entry)

Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological, antiarthritis; antinhemustopicassive; heamostatic; antiathyoid; antidiabetic; noctropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antianaemic; systemic lupus erythematosus; rhemmatoia trihritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogran's syndrome; thyroiditis; systemic vasculitis; autoimmune hemolytic anemia diabetes mellitus; denyemia, immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; untoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease; ss.

99WO-US08615. 99US-0131445. 99US-0132371. 99US-0123618. 99US-0123957. 99US-0125775. 02-MAR-2000; 2000WO-US05841. 99US-0162506. 99US-0128849 99WO-US21547 99WO-US20594 99WO-US20944

99WO-US28313. 99WO-US28409. 99WO-US28301. 0S28551

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421 GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAAT 480
                                                                                                                                                      361 GGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420
                                                                       * 481 IGGIGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCT 540
                                                                                                                                                                                                             541 GCGTTCCCGAACACTAGGCAGCCCCGGGTCTGCACCTCCAAGAGCCCACCTACCACCAG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO1283 (UNQ653) cDNA sequence SEQ ID NO:161.
                                                                                                                                                                                                                                                                                                                                                                              661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
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98US-0098749.
98US-0098750.
98US-0098803.
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98US-0099536.
98US-0099596.
98US-0099602.
98US-0099642.
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980S-0100390
980S-0100584
980S-0100657
980S-0100661
980S-0100664
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98US-0099763.
98US-0099792.
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98US-0099815.
98US-0099816.
98US-0100385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA37071;
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AAA37071
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                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-Dodies, agonists and antagonists are useful for proteins, anti-PRO anti-Dodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic tapper sythematosus, rhematoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sigoren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyellaring diseases of the central and peripheral nervous systems, hepatobilizary diseases, inflammatory concelluseses, inflammatory autoimmune or immune-mediated skin diseases, allergic disease, autoimmune or immune-mediated skin diseases, allergic disease, autoimmune or immune-mediated skin diseases, allergic diseases, autoiming graft rejection and graft-versus host-disease. AMCSB397 to AACSB397 to AACSB397 to AACSB397 to AACSB397 to AACSB57 and AARSB3414 to AARSB3477 represent human PRO polymucleotide and protein sequences given in the sexemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                             Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
                                                                                                                                                                  Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Kabakoff KP, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Stewart TA, Tumas D, Matanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FGGFGFTCACGCTCGGCCTGGCCGCTGCCTTCACCCTGGAGGAGGAGGAGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGAGTTGGAAGTTGGAAGCCACGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IGGGIGTCACGCTCGGCCTGCCGCTGCCTTCCTTCACCCTGGAGGAGGAGATATCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TCACCTICATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCCAGGAGCTGCCCA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GGAGGGACCACTACATTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420
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06-JAN-2000; 2000WO-US00376.

11.FEB-2000; 2000WO-US03565.

18-PEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04444.
                                                                                                                            (GETH ) GENENTECH INC.
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9803-0106464.
9803-0106856.
9803-0106902.
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98US-0106248
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Gaps 9 9 121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180

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Query Match 99.5%; Score 688.8; DB 21; Length 739; Best Local Similarity 99.7%; Pred. No. 2.9e-167; Matches 690; Conservative 0; Mismatches 2; Indels 0;

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181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT

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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primars and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mammalian DNA sequences encoding transmembrane, receptor or secreted PNO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand inheractions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 99; 773pp; English.
9805-0106919.
9805-0106932.
9805-0106934.
9805-010783.
9805-0108779.
9805-010878.
9805-010880.
9805-010880.
9805-010886.
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9805-010886.
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P-PSDB; AAY99389.
   03-NOV-1998

03-NOV-1998

03-NOV-1998

17-NOV-1998

11-NOV-1998

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181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT 240
                      22-MAR - 2001; 2001US - 0816744, 05-APR - 2001; 2001US - 0818366, 10-MAY - 2001; 2001US - 0824208, 10-MAY - 2001; 2001US - 0854208, 25-MAY - 2001; 2001US - 0866024, 25-MAY - 2001; 2001US - 0866034, 30-MAY - 2001; 2001US - 0870574, 30-MAY - 2001; 2001US - 0870574, 30-MAY - 2001; 2001US - 0870574, 30-MAY - 2001; 2001US - 0817443, 30-MAY - 2001; 2001US - 0817443, 30-MAY - 2001; 2001WS - 081749, 20-JUN - 2001; 2001WS - US00000.
                                                                                                                                                                                                                                                           (GERRY) GERRATSER M E.
(GODD), GODDRED A.
(GURN), GURNEY A L.
(HILL), HILLAR K J.
(HARS), MARSTERS S A.
(PANJ), PAN J.
(PADN), PAN J.
(STEP), STEPHAN J F.
(WILL), WILLIAMS P M.
(WOLL), WILLIAMS P M.
                                                                                                                                                                                                       (GETH ) GENENTECH INC. (BAKE/) BAKER K P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosciercosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarterioscierotic; gene; ss.
                                            301 AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCA 360
                           361 GGAGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420
                                                                                 480
                                                                                                 421 GAAAGCTTGTGGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTAAGAAAT 480
                                                                                                                                       TGGTGCAGCGCAAGGGACTCTCGGAGGACGACATTTTCACGCCCTGCAGACGGGAAGCT 540
                                                                                                                                                                                             541 GCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCCACCCTACCACCAG 600
                                                                                                                                                                                                                                                   601 ACACAGAGCCCGGACCACCIGGACCIACCTCCAGCCATGACCCTTCCCTGCTCCCACCC 660
                                                                                                                                                                                                                                                                  421 GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human angiogenesis related cDNA PRO1283 SEQ ID NO: 205.
                                                                                                                                                                                                                                                                                                          661 ACCIGACICCAAATAAAGTCCTICTCCCCCA 692
                                                                                                                                                                                                                                                                                                                        661 ACCTGACTCCAAATAAAGTCCTTTTCCCCCAA 692
                                                                                                                                                                                                                                                                                                                                                                                                        ABL95663 standard; cDNA; 739 BP.
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C2-AUG-2000) 2000US-222695P.

17-AUG-2000) 2000US-04565P.

23-AUG-2000) 2000W0-US23522.

45-AUG-2000) 2000W0-US23522.

07-SEP-2000) 2000WS-US23328.
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2000WO-US32678.
2000US-0747259.
2001US-0757609.
2001US-076498.
2001WO-US66520.
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18-SEP-2000; 2
24-OCT-2000; 2
08-NOV-2000; 2
10-NOV-2000; 2
01-DEC-2000; 2
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22-JAN-2001;
28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
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ABL95663
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BAKER K P. FERRARA N. GERBER H.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGGGTGTCACGCTCGGCCTGGCCTGCTCCTTCACCCTGGAGGAGGAGGATATCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                            One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammmal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 205; 567pp; English.
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P-PSDB; ABB95525.
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ABB18072 to ABIB8258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antinanjongenic, hypotensive, vulneary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
activities, and can be used in gene therapy. The PRO polynucleotides,
cardiovascular, endothelial or angiogenic disorder in a mammal,
e.g. cardiac hypertrophy, trauma, cancer, age-related macular
ce.g. cardiac hypertrophy, trauma, cancer, age-related macular
ce.g. cardiac hypertrophy, trauma, cancer, age-related macular
ce.g. cardiac hypertrophy, mycordial infarctions, thromophlebits,
lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
carcinoma) and wound healing. The PRO polynucleotides have applications
corrictional biology, including use as hybridisation probes, and in
chromosome and gene mapping. ABIR88259 to ABI88267 represent primers and
probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Ferrara N, Gerber B, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
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                                                                                                                                                                                                                                                                                                                       05-APR-2001; 2001US-0828366.
10-MAY-2001; 2001US-0854208.
10-MAY-2001; 2001US-0856280.
25-MAY-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2001; 2001WO-US17443
01-JUN-2001; 2001WO-US17800
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P-PSDB; ABB84919.
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01-DEC-2000; 2
20-DEC-2000; 2
20-DEC-2000; 2
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28-FEB-2001; 2
28-FEB-2001; 2
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09-MAR-2001;
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                                                                                  301 AGCCIGGCAAATACAGCGCCTAIGGGGGGAGGAAGCTCAIGTACCIGCAGGAGCTGCCCA 360
                                                                                                                                                                                                                                                 301 AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAGGTCATGTACCTGCAGGAGCTGCCCA 360
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                                                          241 TCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGG 300
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25-JUL-2000; 2000US-22064P.
28-JUL-2000; 2000WS-220654P.
17-AUG-2000; 2000WS-228695P.
17-AUG-2000; 2000WS-023895P.
24-AUG-2000; 2000WS-053328.
07-SEP-2000; 2000WS-33332B.
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2000US-219556P.
2000US-220624P.
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20-JUL-2000;
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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPID-alpha. OBPs provide long-term retention (gradual capace) of lipophilic compounds, so proflong the 'hold' of perfumes, declarasts etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (aponists or antibodiss) of cabillar librocation receptors; to detect specific artibodies for diagnosis of alleray, astuma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, controlling upperlipidemia or obesity, or to supplement non-maternal milk when combined with untritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for deroxification of the foetus); as a marker of pregnancy or cete. The particular of the foetus); as a marker of pregnancy or cete.
                        New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGGAAGTTGGAAGCCACGTTC 242
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 676 BP; 160 A; 200 C; 204 G; 112 T; 0 other;
                                                                                     Disclosure; Page 113-114; 132pp; French.
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release of perfumes
P-PSDB; AAB67742.
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                                                                                                                                                 301 AGCCIGGCAAAIACAGCGCCTAIGGGGGCCAGGAAGCICAIGIACCIGCAGGAGCIGCCCA 360
                                                                                                                                                                                       GGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420
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                                                                      TCACCITCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGG 300
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/product= "odorant binding polypeptide OBPIIb-alpha"
                  CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT
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Odorant binding polypeptide; ORP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
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/product~ "odorant binding polypeptide OBPIIa-beta"
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   22; Length 676;
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Score 648.8; DB 22
Pred. No. 5.2e-157;
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       Query Match 93.8%;
Best Local Similarity 97.5%;
Matches 659; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human odozant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
       Location/Qualifiers
43..555
/#roduct= "odorant binding polypeptide OBPLIa-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of odorant binding polypeptide OBPIIa-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 676 BP; 158 A; 199 C; 204 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 106-107; 132pp; French.
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                                                                                                                                                                                                                                                                                                                                                                          AAF80039 standard; cDNA; 676 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                           663 CIGACICCAAAIAAAG 678
                                                                                                                                                                                 661 CTGACTCCAAATAAAG 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiallergic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB67738.
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493 540 553

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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPIIa-gamma. OBPs provide long-term retention (gradual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 CTAGGCAGCCCCGGGGTCTGCACCTCCAGAGCCCCACCTACCACCAGAGCACAGAGCCGG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "odorant binding polypeptide OBPIIa-gamma"
                                                                                                                                                                                               423 AAGCTTGTG------GG
                                                                                                                                                                                                                                                                                                                    494 GGGACTCTCGGAGGAGACALTTTCACGCCCCTGCAGGAGGGGAAGCTGCGTTCCCGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of odorant binding polypeptide OBPIIa-gamma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPITa-beta. OBPS provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc. OBP polypeptides are used as binding proteins for hydrophobic lipomas, so prolong the 'hold' of perfumes, appoints or antagonists) of cellular libocalcur receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, compacting the compactions of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, controlling volatilisation of an odorant, specifically in perfumes, controlling pyperlipidemia or obesity, or to supplement non-maternal for treating hyperlipidemia or obesity, or to supplement non-maternal milk when compined with nutritional fatty acids, as food additives; as a transporter of pharmacenticals, especially anticance agents (providing teg. of detoxification of the foetus); as a marker of pregnancy or controlling and as a serial partier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.2%; Score 589.8; DB 22; Length 725; 90.9%; Pred. No. 7.7e-142; tive 0; Mismatches 17; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 725 BP; 163 A; 222 C; 217 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 108-109; 132pp; French.
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Matches 659; Conservative
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P-PSDB; AAB67739.
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release) of lipophilic compounds, so prolong the 'hold' of perfumes, and dedocrants etc.. OBP polypeptides are used as binding proteins for phychophobic liquads (particularly docrants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect to specific antibodies for diagnosis of allergy, asthma or canner; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; or treating hyperlipidemia or obesity, or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as transporter of pharmaceuticals, especially anticancer agents (providing dalyed release) but also for delivery across the placental partier (e.g. for detoxification of the foetus); as a marker of pregnancy or setting incomplemental partier of pharmaceuticals, especially anticancer agents (providing delivery across the placental barrier of percental partier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 ACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGAGGAG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||||
421 AAGCITGIGGCAICIGCICCCIGCAGGGCCGIGCCGCTGICCCCCACGICGGCICACCIGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 -------GGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGA 477
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0; Mismatches 17; Indels 65; Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Score 573.8; DB 22; Length 741;
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88.9%;
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The invention relates to isolated polynuclectide (I) and properiod (II) as useful as hybridisation probes, polyneciase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The complex consists are saylenessed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in madical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. (I) and of the polypectide and polynuclectide sequences have applications in disorders involving aberrant protein expression or biological activity. (I) and of the involving partners are useful in medical disorders involving aberrant protein expression or biological activity. (I) and conduce other types of deat and products dependent on INN and amino acid sequences. Ask6197-Ask94564 represent novel human conductions appeared to the involvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patent did not appear in the printed in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 ATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCTGTCCTTCACCCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.3%; Score 569.2; DB 23; Length 603; ilarity 96.5%; Pred. No. 1.4e-136; Conservative 0; Mismatches 3; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 603 BP; 142 A; 178 C; 182 G; 101 T; 0 other;
                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #11858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did
specification, but was obtained in electroni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but was obtained in electroniat ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 11858; 103pp; English.
                                                                                                    AAS76054 standard; cDNA; 603 BP
721 CCCACCTGACTCCAAATAAAG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang TT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167,
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73.
P-PSDB; ABG11867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 600; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                  13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   11-0CT-2001.
                                                                                                                                        AAS76054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                           RESULT 13
                                                                                 AAS76054
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Pitiot G, Lacazette E, Gachon F;

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Odorant binding polypeptide; OBP; hydrophobic ilgand; odorant; allergy; asthma, cancer; perfume; hyperligidenia, obsity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 GAAGAATTTAAGAAATGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCC 480
                            61 GAGGAGGAGATATCACAGGGACCTGGTAGGAGGCCATGGTGGTGGTGGTGAAGGACTTT 120
                                                                                                                                                       241 ATGCGGAAGACGGAGGGCCTGGCAATACAGCGCCTATGGGGGCCAGGAAGCTCATGTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 CCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG 224
                                                                                                                                                                                                                                                                                                     181 AAGTIGGAAGCCACGTICACCTICATGAGGGAGGATCGGTGCTTCCAGAAGAAATCCTG 240
                                                                                                                                                                                                                                                                                                                                                                 285 ATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCCAGGAAGCTCATGTAC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 GGCCIGCICCACAIGGGAAAGCIIGIGGGIAGGAAIICIGAIACCAACCGGGAGGCCCIG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 CTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAG 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 CCCACCTACCACCAGACACAGAGCCCGGACCACGTGGACCTACCCTCCAGCCATGACCC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 GAGGAGGAGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTGGTAAAGGACTTT 164
                                                                                                                                                                                                                                            225 AAGTIGGAAGCCACGTICACCTICATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 CTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 GAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "odorant binding polypeptide OBPIIb-beta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of odorant binding polypeptide OBPIIb-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF80044 standard; cDNA; 782 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           645 TTCCCTGCTCCCACCCACCTGA 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 TTCCCTGCTCCCACCTGA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-2000; 2000WO-FR02319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-1999; 99FR-0010439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYAU-) UNIV AUVERGNE. (PITI/) PITIOT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200112806-A2
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The present sequence encodes a human odorant binding polypeptide (OBP), assignated OBPILP-beta (long form). OBPs provide long-term retention of gradual release) of lipophilo compounds, so prolong the 'hold' of cardual release) of lipophilo compounds, so prolong the 'hold' of perfumes, deodorants etc.. OBP polypeptides are used as binding proteins to rhydropholo lipands (particularly adorants), as competitive activities of entragonists) of cellular lipocalcin receptors; inhibitors (agonists or antiagonists) of cellular lipocalcin receptors; inhibitors (agonists or antiagonists) of cellular lipocalcin receptors; for controlling volatilisation of an odorant, specifically in perfumes, comments or flavours, e.g. human pheromomes, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; or treating hyperlipidemia or obesity, or to supplement non-maternal milk when combined with nutritional fatty actios, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing transporter or late of or delivery across the placental barrier or cellular late of or delivery across the placental barrier or feet, placental pathology (rupture of the amniotic membrane); and as
                                                                                                                  New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CCTGGCAAATACAGCGCCTGCTTGTCCGCAGTCGAGATGGACCAGATCACGCCTGCCCTC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ATTAGATGGGGCAGGAAGCTCATCATGTACTGCAGGAGCTGCCCAGGAGGACCACTACAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGTGTCACGCTCGGCCTGGCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 AGGAAGCTCTCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCCACGTTC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 ACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 TGGGAGGCCCTAGCCATTGACACATTGAGGAAGCTGAGGATTGGGACAAGGAGGAGCCAAGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 CITITACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 CITITACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GGIGICACGCICGGCCTGGCCGCTGTCCTTCACCCTGGAGGAGGAGGATAICACA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 CCTGGCAAATACAGCGCCT----- 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 ----- 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGCCCAGTGACCTGCCGAGGTCGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 GGGACCIGGIACGIGAAGGCCAIGGIGGICGAIAAGGACITICCGGAGGACAGGAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 560; DB 22; Length 782;
Pred. No. 3.6e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 782 BP; 186 A; 226 C; 239 G; 131 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.9%; Score 560; DB Best Local Similarity 86.4%; Pred. No. 3.6e* Matches 676; Conservative 0; Mismatches
                                                                                                                                                                                                                              Claim 6; Page 115-116; 132pp; French.
                                             WPI; 2001-202864/20.
P-PSDB; AAB67743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiallergic agents.
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437 GAATICTGATACCAACCGGGGGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG 496

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activity, tissue growth factor activity, immunomodulatory activity and activity/infinhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system discoders, arthritis and inflammation.

Note: Records for SRQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACTCTCGGAGGAGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556 AGGCAGCCCCGGGGTCTGCACCTCCAGAGCCCAACCTACCACCAGACACAGAGCCCGGAC 615
                                                                                                                                                                                                                                                                                                                             261 CGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGGAGGAGCCTGGCAAATACAGCGCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 TATEGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 TACTGCAAAGACCAGCACCATGGGGGGCCTCCTCCACATGGGAAAGCTTGTG------ 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 CCTECAGGECCGIGCCGCTGICCCCACGICGCCICACCTGGCCACCTCACCIGCAGGTA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAATICTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGG 495
                                                                                                                                                                                                                                                           GCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAG 140
                                                                                                                                                                                                                                                                                                                                                                          21 GGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTG
                                                                                                                                                                   Query Match 78.6%; Score 543.8; DB 22; Length 781; Best Local Similarity 88.5%; Pred. No. 5.2e-130; Matches 629; Conservative 0; Mismatches 17; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616 CACCIGGACCIACCCICCAGCCAIGACCCITCCCIGCICCCACCCACCIGA 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 781 BP; 172 A; 234 C; 233 G; 142 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell differentiation; gene therapy;
                                                                               600
                                                          556
                                                                                                                            617 ACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCTGACTCCAAATAA 676
                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
           Xu C, Cao Y,
R, Wang ZW;
                                                            ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTA
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Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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CURRENT FILING DATE: 1998-08-05
FATENT FILING DATE: 1997-08-06
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                     GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGACTCTCGGAGGAGGACATTTTC 518
                                                                                            39 CTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 522;
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Pred. No. 1.1e-125;
0; Mismatches 1;
                                                                                                                                                   481 ACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 516
                                                                                                                                   519 ACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 554
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TITLE OF INVENTION: LIPOCALIN HOMOLOG
TITLE OF INVENTION: LIPOCALIN HOMOLOG
TITLE OF INVENTION: LIPOCALIN HOMOLOG
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
REALIER FILING DATE: 1999-08-06
REALIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTHERE: FASLENCY NUMBER: 60/054,867
ANDER OF SEQ ID NOS: 30
SEQ ID NO 1
IENGTH: 522
                                                                                                                                                                                                                              Sequence 1, Application US/09432335
Patent No. 6143720
GENERAL INFORMATION:
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Best Local Similarity 99.8%;
Matches 515; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (7)...(516)
US-09-432-335-1
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ATGIACCIGCAGGAGCIGCCCAGGAGGACCACTACAITITACIGCAAAGACCAGCAC 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 514.4; DB 4;
Pred. No. 1.1e-125;
0; Mismatches 1;
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                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CONCILT, DATE-LI C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
OURRENT APPLICATION NUMBER: US/09/614,022
CURRENT FILING DATE: 2000-07-11
PRIOR PAPLICATION NUMBER: 09/190,663
PRIOR PAPLICATION NUMBER: 09/190,663
PRIOR PRIMED DATE: 1998-08-06
PRIOR RAPLICATION NUMBER: 60/054,867
PRIOR FILING DATE: 1997-08-06
NUMBER: OF SEX ID NOS: 30
SOFTWARE: FASISED for Windows Version 3.0
LENGTH: 522
                    Sequence 1, Application US/09614022
Patent No. 6365716
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OTHER INFORMATION: Degenerate sequence derived from human zlipol OTHER INFORMATION: nucleotide sequence
                                      CORRENT APPLICATION WURBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
CURRENT FILING DATE: 1999-11-02
EARLIER PELING DATE: 1999-08-06
BARLIER PILING DATE: 1999-08-06
BARLIER PLING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASLESQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 510
                                                                                                                                                                                                                                                                                                    NAME/KEY: variation

) LOCATION: (1)...(510)

) OTHER INFORMATION: n is any nucleotide

08-09-432-335-5
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APPLICART: CORLIN: DETFELL C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
APPLICANT: CONKIIN, DAIRELL C. ITLE OF INVENTION: LIPOCALIN HOMOLOG
                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                    FILE REFERENCE: 97-24
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                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Degenerate sequence derived from human 211pol OTHER INFORMATION: nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 53.8%; Score 372.2; DB 3 Best Local Similarity 59.6%; Pred. No. 1.7e.88; Matches 304; Conservative 117; Mismatches 89
                                                                                FACHLER OF OCCUPANT ON THE CONTROL OF STATEMENT CONCILIN, DATECLIN GONOLOG TITLE OF INVENTION: LIPOCALIN GONOLOG FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130,663A
CURRENT FILLING DATE: 1998-08-05
ERALLER APPLICATION NUMBER: 60/054,867
ERALLER PILLING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FESTER OF WINDOWS VERSION 3.0
SEQ ID NO 5
LENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525 CIGCAGACGGGAAGCIGCGITCCCGAACAC 554
                                                                                                                                                                                                                                                                                                                                                                  NAME/KET: variation
; LOCATION: (1)...(510)
; OTHER INFORMATION: n is any nucleotide
US-09-130-663-5
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Patent No. 6143720
GENERAL INFORMATION:
                                             Sequence 5, Application US/09130663A
Patent No. 6020163
                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-432-335-5
                                         US-09-130-663-5
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324 GGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTAC 383
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.8%; Score 372.2; DB 4; Length 510; Best Local Similarity 59.6%; Pred. No. 1.7e-88; Matches 304; Conservative 117; Mismatches 89; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GARGARGARGARATHACNGGNACNTGGTAKGTNAARGCNATGGTNGTNGANGAYAATTY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 CCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG 224
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                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Degenerate sequence derived from human zlipol
OTHER INFORMATION: nucleotide sequence
NAME/KET: variation
1.00ARTON: (1)...(510)
OTHER INFORMATION: n is any nucleotide
US-09-614-022-5
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APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
CURRENT APPLICATION NUMBER: US/09/614,022
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1998-08-06
PRIOR PELICATION NUMBER: 60/054,867
PRIOR PELICATION NUMBER: 60/054,867
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 510
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Patent No. 5843672
GENERAL INFORMATION:
                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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58 GATACCCCAGCCTTGGGAAAGGACACTGTGGCTGTGTCAGGGAATGGTATCTGAAGGCC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 GCTGCCCTGTCCTTCACCCTGGAGGAGGAGTATCACAGGGACCTGGTACGTGAAGGCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 TGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTAT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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FILING DATE:
ALTING DATE:
ALTING DATE:
ALTONING MARCHAILON:
ALTONBEY ARADISATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 6, 207
REFERENCE/POCKET NUMBER: IMI-026CP(IPC-048CP)
FELEPRAN: (617) 227-7400
FELEPRAN: (617) 227-7400
FELEPRAN: (617) 227-7401
FELEPRAN: (617) 227-5941
INFORMATION FOR ESD ID NO: 1:
SEQUENCE CHRARATERISTICS:
LENGTH: 525 base pairs
FERENCE CHRARATERISTICS:
LENGTH: 525 base pairs
FERENCE CHRARATERISTICS:
LENGTH: 525 base pairs
FERENCE CHRARATERISTICS:
ATRANDENNESS: single
STRANDENNESS: SINGLE
FORDINGY: Linear
NUMBER OF SEQUENCES. -
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
STREET: 60 State Street, suite 510
CITY: Boston
STATE: MA
STATE: WA
S
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CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/467,603
FILING DATE: US/08/467,603
FILING PARTICATION 514
PRIOR APPLICATION DATA:
BETING APPLICATION NUMBER: US/08/156,549
FILING DAMP:
                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
// ICCATION: 1..525
// ICCATION: 79..57
US-08-467-603-1
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Gaps

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444 GATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCTGCAGCGCAAGGGACTCTCG 503
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                                                                                                                                                                                                                                          324 GGGGGCAGGAAGCTGATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTAC 383
                                                                                                                                                                                                                                                                                                                                                             292 GAGGGCGAGCGTGTCGTGTCCATCCCGGTCCCGGTGAGGGACCACTACATTCTCTAC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                          384 TGCAAAGACCACCACCACCACTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Morgenstern, Jay P.

APPLICANT: Morgenstern, Jay P.

APPLICANT: Edialdaukas, Christine B.

APPLICANT: Blaindaukas, Christine B.

APPLICANT: Dander and Uses Therefor

NUMBERS OF SEQUENCES: 104

CORRESPONDENCES: LAHIVE & COCKTEELD, LLP

STREET: 28 State Street

CONTRIE: MA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: PROPERTY CONTRIBLED

COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 GAGGAGGACATTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGGA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: READABLE FOUR
MEDIUM TIPE: Ploppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08 491,861A
APPLICATION NUMBER: US/099,712
FILING DATE: 31-Dec-92
ATORNEF/AGENT INFORMATION:
APPLICATION NUMBER: MAY
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATICS:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO:
TELEPRONE: (617) 724-4214
INFORMATION FOR SEQ ID NO:
TEREPRONE (617) 742-4214
INFORMATION FOR SEQ ID NO:
TEREPRONE (717) 742-4214
INFORMATION FOR SEQ ID NO:
TEREPRONE (617) 742-4214
INFORMATION FOR SEQ ID NO:
TEREPRO
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                                           21.0%; Score 145.2; DB 2; Length 525; 60.0%; Pred. No. 4.3e-29; tive 0; Mismatches 178; Indels 9
                                                                                                                                  COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
MEDIDIM TYPE: Floppy disk
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OVERTAING STETEN: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURESHY APPLICATION NUMBER: US/08/466,793
FILING DAFE: 06-UN-1995
CLASSIFICATION NUMBER: US 08/156,549
FILING DAFE: 22-NOV-1993
FILING DAFE: 22-NOV-1993
FILING DAFE: 31-Dec-92
APTORNEY/AGENT INFORMATION:
NAME: MANGER: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: MANGER: 36,207
REFERENCE/FOCKET NUMBER: 36,207
REFERENCE/FOCKET NUMBER: 36,207
TELEFRONG MANGER: 36,207
TELEFRONG (617) 227-7400
TELEFRONG (617) 227-7400
TELEFRONG (617) 227-7401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 Base pairs
LENGTH: 252 Base pairs
TYPE: nucleic acid
STANDENDESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kanleccny, Andrewy
APPLICANT: Ranleccny, Andrewy
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor NUMBER OF SEQUENCES: 104
KOMERSPONDENCES: 104
KOMERSPENDENCES: LAHIVE & COCKPIELD
STREET: 60 State Street, suite 510
GINTEL BOSTON
                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08466793
Patent No. 5891716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.0%
Best Local Similarity 60.0%
Matches 281; Conservative
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79..525
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1..525
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ZIP: 02109
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-466-793-1
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US-08-466-793-1
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62 regalagerererecerenceregagaagarareaeagaaceregarera 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.3%; Score 78; DB 3; Length 147; Best Local Similarity 94.2%; Pred. No. 1.1e-11; Matches B1; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 78; DB 4; Length 147; 94.2%; Pred. No. 1.1e-11; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: CONCILID, DATRELL C.
TITLE OF INVENTION: LIPOCALIN HONOLOG;
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
BARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 06/56,63
EARLIER PILING DATE: 1997-08-06
EARLIER FILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICART: CORLIN, DATFELL C.

TITLE OF INVERTION: LIPOCALIN HOMOLOG

FILE REFRENCE: 97-24

CURRENT APPLICATION NUMBER: US/09/614,022

CURRENT FILING DATE: 1090-07-11

PRIOR APPLICATION NUMBER: 09/130,663

PRIOR APPLICATION NUMBER: 69/054,867

PRIOR PILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                               122 AGGCCAFGGTGGTCGATAAGGACTTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: NEE-tagged linker US-09-432-335-16
                                                                    139 AGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 AGGCCATGGTGGTCGATAAGGACTTT 164
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                                                                                                                                                                                               RESULT 11
US-09-432-335-16
; Sequence 16, Application US/09432335
; Patent No. 6143720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .; Sequence 16, Application US/09614022; Patent No. 6365716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 94.28
Matches 81; Conservative
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US-09-614-022-16
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60.0%; Pred. No. 4.3e-29;
tive 0; Mismatches 178; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                                       84 GCTGCCCTGTCCTTCACCCTGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 143
                                                                                                                                                                                                                                                                                                                                                                       58 GATACCCCAGCCTTGGGAAAGGACACTGTGGCTGTGTCAGGGAAATGGTATCTGAAGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                         144 ATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 Argacadcadaccadgadgraccrga-----gadgccrgacrcagrgacrccargarc 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 GIGACAGCCCIGGGCGGTGGGAAGIIGGAAGCCACGIICACCIICAIGAGGGAGGAICGG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 CTCARAGCCCAGAAGGGGGGCAACCTGGAAGCCAAGATCACCATGCTGACAATGGTCAG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 IGCAICCAGRAGAAAAICCIGAIGCGGAAGACGGAGGAGCCIGGCAAAIACAGCGCCTAI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 TGGCOGCTGCCCTGTCCTCCCTGGAGGAGGAGATCACAGGGACTGGTACGTGA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 GGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 GAGGGCCAGCGTGTTCTTCCAGCCGTCCCGGTGAGGGACCACTACATTCTCTAC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 TGCAAAGACCAGCACCATGGGGCCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 GAGCAGAGCCAAGAGGCCTTGGAGGATTTTCGGGAATTCTCAAGAGCCAAAGGA---TTG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 GAIACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.3%; Score 78; DB 3; Length 147;
Best Local Similarity 94.2%; Pred. No. 1.1e-11;
Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 GAGGAGGACATITICACGCCCTGCAGACGGGAAGCTGCGTTCCCGAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 AACCAGGAGATTTTGGAACTCGCGCAGAGCGAAACCTGCTCTCCAGGA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09130663A
Patent No. 6020163
GENERAL INFORMATION:
APPLICANT: CORKLID, Darrell C,
TITLE OF INVENTION: INFORMATIN HOMOLOG
FITLE REPRENDE: 97-24
CURRENT PAPLICATION NUMBER: US/09/130,663A
CURRENT PAPLICATION NUMBER: 06/054,867
ERALIER APPLICATION BOTE: 1997-08-06
SEALLIER PILING DATE: 1997-08-06
NUMBER OF SEX ID NOS: 30
SOFTWARE: FASASEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: NEE-tagged linker US-09-130-663-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    Matches 281; Conservative
                                                                                                                       mat_peptide
79..525
FEATURE:
NAME/KEY: CDS
TATTON: 1..525
                                                                                                                                                                                                                                               Similarity
                                                                    LOCATION:
FEATURE:
                                                                                                                    NAME/KEY:
                                                                                                                                               ; LOCATION:
US-08-491-861A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9-130-663-16
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67 GETGGTCTGTCCTTGTAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 126
     67 GGTGGTCTGTCCTTCACCCTGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 126
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Best Local Similarity 96.3%; Pred. No. 3.1e-11;
Matches 78; Conservative 0; Mismatches 3; Indels 0; Gaps
                                                                                                                                                                                                Sequence 24, Application US/09614022
Patent No. 6365716
GENERAL INFORMATION:
TITLE OF INVENTION: LIPCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/614,022
CURRENT APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASLESD for Windows Version 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: N-terminal Flag linker US-09-614-022-24
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Job time : 55.2996 secs
                                                                          127 ATGGTGGTCGATAAGGACTTT 147
                                                  144 ATGGTGGTCGATAAGGACTTT 164
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ORGANISM: Artificial Sequence
                                                                                                                                                              RESULT 15
US-09-614-022-24
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62 TGGAAGGTGGTCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGA 121
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Best Local Similarity 96.3%; Pred. No. 3.1e-11;
Matches 7%; Conservative 0; Mismatches 3; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels 0; Gaps
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: LIPOCALIN HOWOLOG
FILE REFERENCE: 97-24
CURRENT PAPLICATION WOMBER: US/09/130,663A
CURRENT FILING DATE: 1998-08-05
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION.
APPLICATE TREORATION.
ITILE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER PILING DATE: 1999-08-06
EARLIER PILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 30
SOFTRARE: FASESEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 24
TEMPORE 10.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: N-terminal Flag linker US-09-130-663-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: N-terminal Flag linker US-09-432-335-24
                                                                ; Sequence 24, Application US/09130663A
; Patent No. 6020163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09432335 Patent No. 6143720
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                              RESULT 13
US-09-130-663-24
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Scoring table:

Searched:

Title: Perfect score:

Run on:

Sequence:

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sequence 1141, App
sequence 1181, A
sequence 11818, A
sequence 59, Appl
sequence 7960, Ap
sequence 7960, Ap
sequence 1855, Ap
sequence 1855, Ap
sequence 17, Appl
sequence 17, Appl
sequence 17, Appl
sequence 17, Appl
sequence 1, Appl
sequence 43, Appl
sequence 43, Appl
sequence 43, Appl
sequence 53, Appl
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APPLICANT: COLENT, MAURICE
APPLICANT: COLENTS, TRACET I.
APPLICANT: COLENTS, TRACET I.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVER C.
APPLICANT: REAGCHVIL, JON D.
APPLICANT: REAGCHVIL, JON D.
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: STROOFE, STEPHEN D.
APPLICANT: STROOFE, STEPHEN D.
APPLICANT: STROOFE, STEPHEN D.
APPLICANT: TYOURE, STEPHEN D.
APPLICANT: TYOURE, STEPHEN D.
APPLICANT: TYOURE, STEPHEN D.
APPLICANT: TYOURE, STEPHEN D.
APPLICANT: TYOURE STEPHEN D.
APPLICANT: TANOURE, STEPHEN D.
APPLICANT: APPORTES, TYOUR C.
APPLICANT: ADDOCT PARK ROAD
CITT: Abbott Park Road
CITT: Abbott Park Road
CITT: Abbott Park
STAFE: IL
COMPUTER USA
ZIP: GONG4-3500
COMPUTER USA
10 US-09-886-055-194

10 US-09-878-774-11281

10 US-09-878-774-11281

10 US-09-878-574-5305

11 US-09-878-574-3305

12 US-09-878-574-3305

13 US-09-818-574-4330

14 US-09-818-574-4330

15 US-09-818-574-4330

16 US-09-931-876-3670

17 US-09-931-876-3670

18 US-09-917-800A,1590

19 US-10-166-359-1

10 US-09-917-800A,1590

10 US-09-917-808

10 US-09-918-91

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/099,823
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION UNUBER: 08/879,354
FILING DATE: 20-JUN-1997
ATTONNET AGENT INFORMATION:
NAME: BGCKET, Charyl L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-09-099-823-4
        00000
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Sequence 5, Appli
Sequence 10, Appli
Sequence 803, Appli
Sequence 1747, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 237, Appl
                                                                                                                                                                                  February 9, 2003, 21:14:50 ; Search time 53.348 Seconds
(without alignments)
6148.496 Million cell updates/sec
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                                                                                                                                                                                                                                                                                         US-09-099-823-4
692
1 GACGCOCAGTGACCTGCCGA......ATAAAGTCCTTCTCCCCCCA 692
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1: /cgn2_6/ptodata/l/pubpa/US01_PUBCOMB.seq:*

2: /cgn2_6/ptodata/l/pubpa_PCT.NEW_PUB.seq:*

3: /cgn2_6/ptodata/l/pubpa_VES0_EUBCOMB.seq:*

4: /cgn2_6/ptodata/l/pubpa_PCTUS_PUBCOMB.seq:*

5: /cgn2_6/ptodata/l/pubpa_PCTUS_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/l/pubpa_PCTUS_PUBCOMB.seq:*

14: /cgn2_6/ptodata/l/pubpa_PCTUS_PUBCOMB.seq:*
                                   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-99-823-5

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10 US-09-99-823-3

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10 US-09-98-84-847-1

10 US-09-854-847-1

10 US-09-854-847-1

9 US-10-121-044-237

9 US-10-121-044-237

9 US-10-121-044-237

9 US-10-121-044-237

10 US-09-884-847-137

10 US-09-884-847-137

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10 US-09-884-847-137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               408267 seqs, 237001491 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                         nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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746.3
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Database :

Score

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181 CCAGGAAGGIGTCCCCAGTGAAGGIGACACCCTGGGCGGTGGGAAGTTGGAAGCCACGT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IGGGFGTCACGCTCGGCCTGCCTGCCTCTCTCACCCTGGAGGAGGAGGATATCA 120
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                                                     APPLICANT: FALLBANA, FALDANA, ADULA NA APPLICANT: FALLBANA, FALDANA, ADULA NA APPLICANT: GORDON, UULIAM APPLICANT: GORDON, UULIAM APPLICANT: GORDON, UULIAM CAPLICANT: HODGES, STEVEN C. APPLICANT: RARGORYL, ON D. APPLICANT: RARGORYL, CHRISTI APPLICANT: STEPPEL, CHRISTI APPLICANT: STEPPEL, CHRISTI APPLICANT: TU, HONG TITLE OF INVENTION: REAGENTS AND METHODS USEFUL TITLE OF INVENTION: REAGENTS AND METHODS USEFUL TITLE OF INVENTION: POR DETECTING DISEASES OF THE BREAST NUMBER OF SEGURACES: 27 CORRESPONDENCES ADDOCT LABORATORIES ADDOCT LABORATORIES ADDOCT LABORATORIES ADDOCT PARK ROAD CITY: ADDOCT PARK ROAD CITY: ADDOCT PARK RABABILE FORM: MEDIUM TYPE: DISKCTLE COMPUTER IEM COMPATIBLE OF SETENDALIE FORM: MEDIUM TYPE: DISKCTLE COMPUTER IEM COMPATIBLE OF SETENDALIE FOR WINDOWS VERSION 2.0 SUCHWARDEN SETENDALIE FOR WINDOWS VERSION 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UTN-1997
ATTORNEY/ACENT INCORNATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 847/938-1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823
FILING DATE:
               COLPITYS, TRACEI L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 692; Conservative
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US-09-099-823-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 regerercacercececrescerecerecerrercerecerseageagearearea 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TCACCITCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGGGG 300
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                            Length 692;
                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                              Ouery Match 100.0%; Score 692; DB 10; Best Local Similarity 100.0%; Pred. No. 1.7e-173; Matches 692; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 ACCEGACTCCAAATAAAGTCCTTCTCCCCCCA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
     REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.Pl
TELECOMMUNICATION INFORMATION:
TELEFRONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09099823
Patent No. US200200018990A1
APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                                     INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHRACKTRISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                  ;
TOPOLOGY:
US-09-099-823-4
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; TYPE: DNA; ORGANISM: HOMO Sapiens
US-09-833-381-803
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US-09-833-381-803/c
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                                                                                                                                                                                                                               GGAGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGGCCTGCTCCACATGG 420
                                                     GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAAT 480
                                                                                              0; Gaps
                                                                                                                                                                                                                   601 ACACAGAGCCGGGACCACCIGGACCIACCCTCCAGCCATGACCCTTCCCTGCTCCCACCC
301 AGCCIGGCAAAIACAGCGCCIAIGGGGGCAGGAAGCICAIGIACCIGCAGGAGCIGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Watch 74.3%; Score 514.4; DB 10; Length 523; Best Local Similarity 99.8%; Pred. No. 1.1e-126; Matches 515; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOK, Si
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Followay, James L.
FILE REFERENCE: 00-85
CURRENT APPLICATION UNBER: US/09/951,845
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                               ACCIGACICCAAAIAAAGICCITCICCCCCCA 692
                                                                                                                                                                                                                                                                            661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09951845 Patent No. US20020098497A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KET: CDS
; LOCATION: (8)...(517)
US-09-951-845-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523
                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-951-845-1
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SEQ ID NO 1
LENGIH: 52
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Sequence 803, Application US/0983381

Fatent No. US20020132090a1

Patent No. US20020132090a1

GENERAL INFORMATION:

APPLICANT: ROBISON, Reith E.

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT PILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR APPLICATION NUMBER: 09/516,448

NUMBER OF ED NOS: 2050

NUMBER OF ED NOS: 2050

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: AND 08 093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 GIGICCCCAGIGAAGGIGACCTIGGCCGGGGGAAGIIGGAAGCCACGIICACCIIC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 ATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGGC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 AAAIACAGCGCCIAIGGGGGGAAGCACAAGTACCIGCAGGAGCIGCCCAGGAGGAC 368
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279 ATCCTGATGCGGAAGACGGAGGCCTGGCAAATACAGCGCCCTATGGGGGGAAGGTC 338
                                                                   398
                                                                                                                                     399 CATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAG 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 483.6; DB 10; Length 501;
Pred. No. 1.5e-118;
0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                              519 ACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 554
                                                                                                                                                                                                                                                                                                #82 ACCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.9%;
Best Local Similarity 99.0%;
Matches 497; Conservative
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us-09-099-823-4.rnpb

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APPLICANT: Robison, Reith E. TITLE OF INVERTION: No. US20020132090Alel Nucleic Acid and Protein Homologs FILE REFERENCE: 5800-119
CURRENT RILLIG DATE: 2001-04-11
FRIOR APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
   414 CACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTT 473
                                             277 CACATGGGAAAGCTTGTGGGGTAGGAATTCTGATACCCACCGGGAGGCCCTGGAAGATTT 218
                                                                                                                               474 AAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACG 533
                                                                                                                                                                        534 GGAAGCTGCCGTTCCCGAACACTAGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCTA 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT 240
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                                                                                                                                                                                                                                                                                                97 CCACCAGACACAGAGCCGGGACCACCCTCCAGCCAGCCATGACCTTCCCTGCT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ACGCCCAGTGACCTGCCGAGGTCGGCAGCACACACTCTGGAGATGAAGACCCTGTTCCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match. 42.8%; Score 296; DB 10; Length 336; Best Local Similarity 99.4%; Pred. No. 4.1e-69; Matches 318; Conservative 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          654 CCCACCCACCTGACTCCAAATAAAGTCCTTCTCCCCC 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 CCCACCCACCTGACTCCAAATAAAGTCCTTCTCCCCC 1
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1747
LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1747, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) TYPE: DNA
) ORGANISM: Homo sapiens
US-09-833-381-1747
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US-09-833-381-1747
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354 CTGCCCAGGAGGACCACTACATTTACTGCAAAGACCAGCACCATGGGGGCCTGCTC 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: COLDITIES, TRACET L.
APPLICANT: GONDITIES, TRACET L.
APPLICANT: GONDON, UTLAN
APPLICANT: GONDON, UTLAN
APPLICANT: GRANADOS, EDRAND N.
APPLICANT: HONGES, STEVEN C.
APPLICANT: KLASC, MICHAEL R.
APPLICANT: KRANCGFUL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: TY, HONG
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
KNUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 337;
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Best Local Similarity 100.0%; Pred. No. 6.2e-80;
Matches 337; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATE:
CLASSIFICATION DATE:
CLASSIFICATION DATE:
FILNG DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/879,354
FILNG DATE: 20-UUN-1997
ATTORNEY APPRICATION:
WANTED DATE: APPLICATION:
AND APPLICATION DATA:
APPLICATION UNBER: 08/879,354
ATTORNEY APPLICATION:
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REGISTRAMION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.Pl
TELECOAMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BILLING-MEDEL, PATRICIA APPLICANT: COBEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 27
CORRESPONDENCE STADRESS:
ADDRESSES: Abbort Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STAFE: 110
                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09099823 Patent No. US20020018990A1 GENERAL INFORMATION:
                                                                                                                               669 CCAAATAAGTCCTTCTCCCCC 690
                                                                                                                                                                        22 CCAAATAAAGICCTICTCCCCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 847/938-2623
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US-09-099-823-3
                                                                                                                                                                                                                                                                                 RESULT 5
TS-09-099-823-3/c
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353 GCTGC 357

Patent No. US20020018990A1

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61 IGGGIGTCACGCICGGCCTGCCCTGCCCTGTCCTTCACCCTGGAGGAGGAGGAIAICA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACGCCCAGTGACCTGCCGAGGTCGGCACACACACACGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GACGCCCAGTGACCTGCCGAGGTCGGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.1%; Score 236; DB 10; Length 236; Best Local Similarity 100.0%; Pred. No. 2.5e-53; Matches 236; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: YU, HONG
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCISS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFWRARE: PASTERM FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6120.US.P1
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CIASSIFICATION:
FRICK APPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-JUN-1997
ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl Li,
REGISTRATION NUMBER: 35,441
REFERENCE, COCKET NUMBER: 6120.US.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                   Sequence 1, Application US/09099823
Patent No. US20020018990A1
                                                                                                                                                                                                                                        COHEN, MAURICE
COLPITIS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                         GRANADOS, EDWARD N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                  ORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-099-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60064-3500
241 GCTGC 245
                                                                                   RESULT 8
US-09-099-823-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AGCCACGITCACCITCATGAGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 CAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 | GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTGGTCGATAAGGACTTTCCGGAGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.4%; Score 245; DB 10; Length 245; Best Local Similarity 100.0%; Pred. No. 1.1e-55. Matches 245; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                THE BREAST
                                                                                                                                                                                                           APPLICANT: KRATOCHVII, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: SCHEFFEL, CHRISTI
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: TU, HON STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: POR DETECTING DISEASES OF THE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY: USA

COUNTY: USA

COMPUTER REACHSIDE FORM:
MEDIUM TIPE: Diskette
COMPUTER: IBM COMPALINE
COMPUTER: IBM COMPALINE
COMPUTER: TBM COMPALINE
COMPUTER: TBM COMPALINE
COMPUTER: TBM COMPALINE
COMPUTER: TBM COMPALINE
CONTREM APPLICATION DATA:
FILING DATE:
CLASSIFICATION NUMBER: US/09/099,823
FILING DATE:
CLASSIFICATION NUMBER: 08/879,354
FILING DATE: 20-UUN-1997
APPONENT IMPORATION:
COMPANDIATE: AD-UN-1997
APPONENT IMPORATION:
COMPANDIATE: AD-UN-1997
APPONENT IMPORATION:
COMPANDIATE: AD-UN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6120.US.P1
              BILLING-MEDEL, PATRICIA COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                         COLPITY, TRACET L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANDOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Becker, Cheryl L.
REGISTRAITON NUMBER: 35,441
REFERENCE/POCKET NUMBER: 6120
TELECOMUNICATION INFORMATION:
TELEPRONE: 847/935-1729
TELEPRONE: 847/935-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 base pairs
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US-09-099-823-2
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Sequence 1, Application US/10143576

Publication No. US20030013151A1

GENERAL INFORMATION:
APPLICANT: HU, SONG et al.
APPLICANT: HU, SONG et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF

FILE REPERANCE: CLO01237

CURRENT APPLICATION NUMBER: US/10/143,576

CURRENT APPLICATION NUMBER: 2002-05-13
                                            264 TGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTAT 323
                                                                                                                                                                                                                                                                                                                                                                                          324 GEGEGCAGGAAGCICATGIACCIGCAGGAGCIGCCCAGGAGGGACCACTACAITITAC 383
                                                                                                                                                                                                                 384 TGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCT 443
                                                                                                                                                                                                                                                                                                     444 GATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGG---TGGTCGATAAGGAC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 AIGAAGACCCIGITCCIGGGTGTCACGCTCGGCCTGCCGCTGCCCTGTCCTTCACCCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 TITCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 GGGAAGTIGGAAGCCACGTICACCTICATGAGGGAGGATCGGIGCATCCAGAAGAAAAIC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 GECGCCCICCACCICCACATGGAGTICCCGGGGGGGGGGGCTGTAACCAGGTGGAIGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATG---GGGGCAGGAAGCTC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 GACTACCTGAAGGTGGGCTCCGAGGGACACTTCAGAGTCCCGGCCTTGGGCTACCTGGAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 ATGIACCIGCAGGAGCIGCCCAGGAGGGACCACIACAICITITACIGCAAAGACCAGCAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 gridoscarcorsidadadadadadacorcorrosconorrandarcarcandadoscong 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 54.8; DB 9; Length 55
46.6%; Pred. No. 2.1e-05;
Live 0; Mismatches 277; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 GAGGAGGACATITICACGCCCTGCAGACGGGAAGCTGCGTTCCCGAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 AACCAGGAGATTTTGGAACTCGCGCAGAGCGAAACCTGCTCCTCCAGGA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.9%
Best Local Similarity 46.6%
Matches 247; Conseyvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-143-576-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-143-576-1
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84 GCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 ATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                                           APPLICANT: Morgenstern, Jay P.
APPLICANT: Raid-corny, Andrzey
APPLICANT: Bliindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.08; Score 145.2; DB 10; Length 525; Best Local Similarity 60.08; Pred. No. 2.9e-29; Matches 281; Conservative 0; Mismatches 178; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILLING DATE:

AFALLING DATE:

NAME: MANGER: MANGRADION:

NAME: MANGRAGH SANY BE

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)

TELEPRONE: (617) 227-7400

TELEPRONE: (617) 727-7400

TELEPRONE: (617) 747-4214

INFORMATION PROPERSION: (617) 747-4214

INFORMATION POR SEQ ID NO: 1:

SEQUENCE CHRACTERISTICS:

LENGTH: 525 base pairs

TYPE: INCIDIO COLD

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKTIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,671
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REDIUM TYPE: Floppy disk COMPUTER: IBM PC. COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII-+px+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 08/491,861
FILING DATE:
                                                                                                                                                                                                                                       Sequence 1, Application US/09374671 Patent No. US20020012963A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | NAME/KEY: CDS
| LOCATION: 1..525
| FEATURE:
| NAME/KEY: mat_peptide
| LOCATION: 79..525
| US-09-374-671-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                               RESULT 9
US-09-374-671-1
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6; Gaps

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Sequence 9, Application US/09854847

Sequence 9, Application US/09854847

GENERAL INFORMATION: A Lexander Jr.

APPLICANT: Matther, C. Alexander Jr.

APPLICANT: Matther, C. Alexander Jr.

TILE REFERENCE: LEX-0173-USA

CURRENT FAPLICATION NUMBER: US/09/854,847

CURRENT FAPLICATION NUMBER: US/09/854,847

CURRENT FILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTC 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 Generida a de controca de actrica a consecue de descrica de descritor de descritor de de controca de descritor de de descritor de d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 GAGGAGGAGATATCACAGGGACCTGGTAACGTGAAGGCCATGG---TGGTCGATAAGGAC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 TITCCGGAGGACAGGAGGCCCAAGGAAGGTGTCCCCAAGTGAAGGTGACAGCCCTGGGCGGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 GGGAAGTIGGAAGCCACGTICACCIICAIGAGGAGGAGGAICGGIGCAICCAGAAGAAAAIC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 CIGAIGCGGAAGGAGGAGCAGCAAAAAACAGCGCCIAIG---GGGGCAGGAAGCIC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AIGIACCIGCAGGAGCIGCCCAGGAGGGACCACIACAICIITIACIGCAAAGACCAGCAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 CAIGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519 ACCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGG 568
505 ATGCTGCCCCAGTCAGATGCATGCAACCCTGAGAGCAAGGAGGCGCCCTG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54.8; DB 10;
Pred. No. 2.1e-05;
0; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09854847
Patent No. US20020107375A1
GENERAL INFORMATION:
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Best Local Similarity 46.6%;
Matches 247; Conservative 0
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; ORGANISM: homo sapiens
US-09-854-847-9
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US-09-854-847-17
                                                                                                 RESULT 12
US-09-854-847-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20020107375Alel Human Lipocalin Homologs and Polynucleotide
PLICE REFERENCE: LEA 1979-USA
CURRENT APPLICATION NUMBER: US/09/854,847
PRIOR APPLICATION DATE: 2001-09-10
PRIOR APPLICATICATICATION NUMBER: US 60/203,874
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                        459 GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTC 518 .
                                                                                  385 GAGGGGGCCTCAGCACCATGCTGCTACAGCCGGACCCCAGGATGTGAGTCCCCCAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 ITTCCGGAGGACAGGACCCCAGGAAGGTGTCCCCCAGGAAGGTGACAGCCCTGGGCGGT 221
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                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENOTH: 555
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Patent No. US20020107375A1
GENERAL INFORMATION:
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; ORGANISM: homo sapiens
US-09-854-847-1
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CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
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PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-27
PRIOR PRILICATION NUMBER: 60/063327
PRIOR PLILING DATE: 1997-10-27
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PRIOR PLILING DATE: 1997-10-29
PRIOR FILING DATE: 1997-10-29
PRIOR PLILING DATE: 1997-10-29
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PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILLING DATE: 1997-09-17
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FILING DATE: 1997-09-18
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FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
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     Watanabe,Colin
Wood,William
                                                                                                APPLICANT: Zhang
TILE OF INVENTION:
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FILE REFERENCE: LEX-0173-USA
CURRENT APPLICATION NUMBER: US/09/854,847
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 60/203,874
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 17
ERONE FEASERS for Windows Version 4.0
SEQ ID NO 17
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Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: homo sapiens
US-09-854-847-17
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US-10-028-072-237
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PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/08106

PRIOR PRILICATION NUMBER: 60/08106

PRIOR PLING DATE: 1988-06-01

PRIOR PLING DATE: 1988-06-10

PRIOR PLING DATE: 1998-06-10

PRIOR PLING DATE: 1998-06-10

PRIOR PLING DATE: 1998-06-10

PRIOR PLILING DATE: 1998-06-10

PRIOR PLILING DATE: 1998-06-11

PRIOR PLILING DATE: 1998-06-11

PRIOR PLILING DATE: 1998-06-11

PRIOR PLILING DATE: 1998-06-17

PRIOR PLILING DATE: 1998-06-19

PRIOR PLILING DATE: 1998-06-19

PRIOR PLILING DATE: 1998-06-19

PRIOR PLILING DATE: 1998-06-24

PRIOR PLILING DATE: 1998-07-02

6; Length 762; Ouery Match 7.7%; Score 53.2; DB 9; Length 76
Best Local Similarity 46.4%; Pred. No. 6.1e-05;
Matches 246; Conservative 0; Mismatches 278; Indels

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410 GAGGGGGCCTCAGGACCATGGTGCAGCTCTACAGCCGGACCCAGGATGTGAGTCCCCAG 469 50 Arcercaccercerceccacceccacaccercaccercaccercecercecaccecercecerce 109 105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGG---TGGTCGATAAGGAC 161 222 GGGAAGTTGGAAGCCACGTTCACCTTCATGAGGAGGATCGGTGCATCCAGAAGAAAATC 281 282 CIGAIGCGGAAGACGGAGGAGCCIGGCAAAIACAGCGCCIAIG---GGGGCAGGAAGCIC 338 290 GAGTACCTGAAGGTGGGCTCCGAGGGACACTTCAGAGTCCCGGCCTTGGGCTACCTGGAC 349 339 ATGIACCIGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTACTGCAAAGACCAGCAC 398 399 CATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGGTAGGAATTCTGATACCAACCGGGAG 458 GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTC 518 45 ATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGTGCCCTGTCCTTCACCCTG 104 162 TITCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGT 221 459 g δŏ 셤 ŏ 셤 Ω qq ğ 셤 ŏ à 셤

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFEFTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE REFERENCE: P3330RL017
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DAIE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
ENGINE OF 237
ENGINE 757
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Best Local Similarity 46.4%; Pred. No. 6.1e-05;
Matches 246; Conservative 0; Mismatches 278; Indels 6; Gaps
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                       Sequence 237, Application US/10121049 Publication No. US20030022239al GENERAL INFORMATION:
                                                                                                                                                                                                  CANT: Barer, Kevin P.
CANT: Beresini, Maureen
CANT: DeForge, Laura
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                         rney, Austin L
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US-10-121-049-237
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QY 459 GCCTGGAAGAATTAAGAAATTGGTGCAGCGCAAGGACTCTCGGAGGAGACATTTTC 518
Db 470 GCTTGAAGTCCTTCCAGAACTTCTACCGAACCTCGGGGCTCCCCAAGAAATGATGGT 519
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Search completed: February 9, 2003, 22:08:31 Job time: 58.348 secs

⁵¹⁹ ACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGG 568

48.7 337 9 AAA60323 B A 47.6 349 9 A1143970 B 47.6 349 9 A1143970 B 51259 B 51259 B 51259 B 512 8 512	8.0 7.7 7.4 7.4 7.4 7.4 7.0 8.9 6.9 6.8 6.8 6.8 6.6 6.6 6.6 6.6 6.6 6.6 6.6	6.4 339 6.4 4339 6.4 6.4 551 6.4 663 6.4 663 6.4 865 6.4 875 6.4 538 6.4 538 6.4 538 6.4 538 6.4 538 9.4 538	AW5 xo4 sim seq AW5 AW5 AW5 EST hum Hom	1 (bases I to 532) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap. Tumor Gene Index Tumor Gene Index Uppublished (1997) Contact: Robert Strausberg, Ph.D. Rmail: Gapple-rémail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDMA Library Preparation: Life Technologies, Inc. CDMA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Rashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiMi at:
	23 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 AM513637/c LOCUS DEFINITION DEFINITION ACCESSION VERGION VERGION VERGION CETWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT
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pugen Ltd. pugen Ltd. arch time 1923.58 Seconds out alignments) 269 Million cell updates/sec	ATAAAGICCITCTCCCCCA 692 es 32308132			ed by chance to have a f. the result being printed, ore distribution. Description AWT13637 xc47h10.x AWT7608 on61e03.s AL219510 qh2402.x AA460385 xx51e06.r AA936288 on75f11.s
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd OM nucleic - nucleic search, using sw model Run on: February 9, 2003, 22:05:30 ; Search time 5826.269 Millign	Title: US-09-099-823-4 Perfect score: 692 Sequence: 1 GACGCCCCAGTGACCTGCCGAATAAAGTCCTTCTCCCCCCA 692 Scoring table: IDENTITY.NUC Gapop 10.0 , Gapext 1.0 Searched: 16154066 seqs, 8097743376 residues Total number of hits satisfying chosen parameters: 32308132 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%	Database: EST:* Database: EST:* 1: em_estba:* 2: em_estbum:* 3: em_estin:* 4: em_estin:* 5: em_estov:* 6: em_estpo:* 7: em_estpo:* 8: em_htc:* 9: 9D_est1:* 10: 9D_est2:* 11: 9D_htc:* 12: 9D_est3:*	13: 90_est5:* 14: 90_est5:* 15: en_estom:* 17: 90_gss:* 18: en_gss.hum:* 19: en_gss.hum:* 20: en_gss.pln:* 21: en_gss.hum:* 22: en_gss.hum:* 23: en_gss.hum:* 24: en_gss.hum:* 25: en_gss.hum:* 27: en_gss.hum:* 27: en_gss.hum:* 27: en_gss.hum:* 27: en_gss.hum:*	Pred. No. is the number of results predicted score greater than or equal to the score of and is derived by analysis of the total score and is derived by analysis of the total score. SCOMMARIES Result No. Score Match Length DB ID C 1 409 72.1 532 10 AWR13637 C 2 465 67.2 513 9 A9377608 C 3 460.6 66.6 477 9 A1221747 C 4 452 8 65.4 449 9 A1219510 S 410.4 59.3 415 9 AA460385 C 5 375 54.2 431 9 AA936288

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1 (bases 1 to 513)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This Consortium (info@image.llnl.gov) for further information.

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Seg primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 339.
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133 c 158 g 134 t

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    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /clone="IMAGE:1561180"

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Unpublished (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 AGTIGGAAGCCACGTICACCTICATGAGGAGGATCGGTGCATCCAGAAGAAAATCCTGA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.1%; Score 499; DB 10; Length 532;
Best Local Similarity 96.8%; Pred. No. 2.6e-110;
Matches 508; Conservative 0; Mismatches 17; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 CGGAGGACAGGAGGCCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 IGCGGAAGACGCAGGAGCCIGGCAAAIACAGCGCCIAIGGGGGCAGGAAGCICAIGIACC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGG 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 TGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586 CCACCCTACCACCACACACAGGCCCGGACCACCTGGACCTACCCTCCAGCCATGACCCT 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 bp mRNA linear EST 26-AC OOGENS.156138.0 3 similar to TR:063613 Q63613 ODORANT-BINDING PROTEIN. , mRNA sequence. AA977608 AA977608 GI:3155054 EST.
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Possible reversed clone: polyT not :Seq primer: -400F from Gibco High quality sequence stop: 316. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        87
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AA977608/c
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Another Organisation of the property of the pr
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1 (bases 1 to 49)
NOI-GARP http://www.ncbi.nlm.nih.gov/ncicgap.
NOI-GARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Uppblished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL ; contact the
This Consortium (infoétinge.llnl,gov) for further information.
Insert Length: 536 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 330.
Location/Qualifiers
                                                                                                    586 CCACCCTACCACCACACACACAGAGCCCGGACCAGGACCTACCCTCCAGCCATGACCCT 645
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195 CCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTCATGAGG 254
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                                                                                                                                       Score 452.8; DB 9; Length 499;
Pred. No. 3.8e-99;
0; Mismatches 29; Indels 0;
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                                                                                                                                                                                                                                       646 TCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
                                                                                                                                                                                                                                                                          1. .499
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IRAGE:1845603"
/clone=lib="Soarse_NFL_T_GBC_S1"
/lab_host="DHIOB"
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135 c 151 g 126 t
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Best Local Similarity 94.2%;
Matches 469; Conservative (
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AI219510/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Add. Lost. Dation of the Actor: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco Ri; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NOHL)9W, testis NNT, and B-Cell libraries (fetal lung NOHL)9W, testis NNT, and B-Cell NCI_CGAP_CCBl) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PGR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726468728711, and 729065-731399. Subtraction by Bento Scares and M. Fettima Bonaldo. "
                                                                     qh90f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNa clone PRAGE:184287 3' similar to TR:Q63613 Q63613 ODORANT-BINDING A1251747, inRNa sequence.
A1251747, 1 GI:3848276
EST.
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Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)

NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Ompublished (1997)

Ompublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbarfemil.nih gov
This clone is available royalty-free through LLNL; contact the
THASC Consortium (info@image.llnl.gov) for further information.
Seq priner: -400F from Globo.
High quality sequence stop: 396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 TGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGCTCATGTACC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 TGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGG 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:1854287"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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/db xref="taxon:9606"
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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 431)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

I Uppublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: ogapbs-rémail.inh.gov
Phis close is available royalty-free through LINL; contact the This close is available royalty-free through LINL; contact the Seq primer: -40miliable organization and an anassham
High quality Sequence stop: 344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 bp mRNA linear EST 29-APR-1998 on 075f11.s1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562541 3' similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN: ;, mRNA sequence. AA936288 AA936288 I GI:3094206 BST.
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(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pr773 vector. Library went through one round of normalization to Cot5, and was constructed by Bentos Coarres and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 AAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGC 336
                                                                                                                                                                                                                                                                                                                                    337 TCATGIACCIGCAGGAGCTGCCCAGGAGGGACCACIACAICTITIACIGCAAAGACCAGC 396
                                                                                                                                                                                                                                                                                                                                                              64 TCATGTACCTGCAGGAGCTGCCCAGGAGGACCACTACATTTACTGCAAAGACCAGC 123
                                                                                                                                                                                                                                                                                                                                                                                                                            397 ACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 AGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 TCACGCCCCTGCAGACGGGAAGCTGCGTTCCCCGAACACTAGGCAGCCCCCGGGTCTGCAC 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AADACCTGATGCGGAAGACGGAGGACCTGGCAAATACAGGGCCTATGGGGGCAGGAAGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.3%; Score 410.4; DB 9; Length 415; Best Local Similarity 99.8%; Pred. No. 6.4e-89; Matches 411; Conservative 0; Mismatches 1; Indels 0.
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//organism="Homo sapiens"
//organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="Taxon:156581"
//clone=lib="Soares_NFI_T_GBC_S1"
//ab_host="DH108"
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AA936288/c
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El (Dassel I to Allan, M. Jennes, L., Dubuque, T., Geisel, G., Jost, S., Kuchas, T., Largy, M., Le, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tennen, R., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Tan, F., Theising, B., White, Y., Wylle Gostler Est Project 1997

Unpublished (1997)

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This clone is wavilable royalty-free through LiAL; contact the
This clone is wavilable royalty-free through LiAL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is
Seq primer. 20mil rev2 ET from Amersham.
Location/Qualifiers
                                                                               319 GECTITIACEGCAAAGACCAGCGCCGEGGGCCTGCGCTACAEGGGAAAGCTEGEGGT 260
       434
                                                                                                                                                                    435 AGGAATTCTGATACCAACCGGGGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAG 494
                                                                                                                                                                                                                             495 GGACTCTCGGAGGAGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 554
                                                                                                                                                                                                                                                                                                                       555 TAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCTACCACCAGACACAGAGCCCGGA 614
                                                                                                                                                                                                                                                                                                                                         Double-stranded cDNA was ligated to Eco RI adaptors
                                                   375 ATCITITACIGCAAAGACCAGCACCAIGGGGCCTGCTCCACAIGGGAAAGCTTGTGGGT
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/db_xref="GDB:6039283"
/db_xref="taxon:9606"
/clone="IMAGB:795778"
/clone_lib="Soares_testis_NHT"
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AA460385.1 GI:2185598
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 349)
Tel: 314 286 1800

Fax: 314 286 1810

Fax: 314 286 1810

This: est-deateon.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infocimage.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seg primer: -41ml3 fwd. Fr from Amersham

High quality sequence stop: 323.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 CACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 AAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACAFTTTCACGCCCCTGCAGACG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 GGAAGCIGCGIICCCGAACACIAGGCAGCCCCGGGGICIGCACCICCAGAGCCCCACCCIA 593
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                                                                                                                                                                                                                                                                                                         1. 337
/organism="Homo sapiens"
/db_xref="GDB:6039283"
/db_xref="taxon:9606"
/clone="IMAGE:795778"
/clone="IMAGE:Cestis_NHT"
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/lab_host="DH10B"
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AI143970.1 GI:3665779
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       Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBEL19W, testis NHT, and B-cell NCI_GGAP_GGB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.B. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Scares and M. Fatima Bonaldo. I others
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1 (basea; 1 to 33).

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Schellenberg, K., Steptoe, M., Tan, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle Wash, Warts Expron. R. and Wilson, R.

Onpublished (1997)

Onchaci: Wilson RX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 CGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 CGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACTGAGGAGCCTGGCAAATTCAGCGCC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 TATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 TACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAAT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 TCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 TCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561 GCCCCGGGTCTGCACCTCCAGAGCCCACACCTACCACCAGACACAGAGCCGGGACCACT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCTGACTCCAAATAAAGTC 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AA460323.1 GI:2185139
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Gaps

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Length 337;

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Enail: genome-reségac.riken.go.jp,
URL:http://genome-reségac.riken.go.jp,
URL:http://genome-gac.riken.go.jp,
Garninci.p., Shibata.g. ar. Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
Garninci.p., Shibata.g. and Bayatsu.N., Sugahara,Y., Shibata,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cONA libraries for rapid discovery of new
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cond
                                                                                                             Arakawa,T., Carnici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramato,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Kohoo,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shiberta, K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
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nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizaw
.K., Fukda, S., Bara, A., Itoh, M., Kawai, J., Shibata, K. and
Bayashizaki, Y.
              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 603)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maysauration. Computational hallysis of Full-Length Mouse cDNAs Compared with Euman Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/db_xref='taxon:10090"
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/clone_lib="RIKEN full-length enriched, 6 days neonate
                                                                                                                                                                                                                                                                                                                                       RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
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                                                                                                                                                                                                                                               cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington Wilversliv Genome Sequencing Center
DNA Sequencing by: Washington Wilversliv Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be
Ground through the I.M.A.G.E. Consortium/LIML at:
Www-bio.llnl.gov/bhpp/image/shminge.html
Seq primer: -40ml3 Fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/13 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 80 c 115 g 99 t
                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-rfemil.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Patima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB618259 603 bp mRNA linear EST 26-0CT-2001
BB618259 RIKEN full-length enriched, 6 days neonate head Mus
musculus CDNA clone 5430417003 5', mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Oppublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 GGGARAGCTTGTGGGTAGGRATTCTGATACCARCCGGGAGGCCCTGGRAGARTTTAAGAA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 ATTIGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 CIGCGITCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACC 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.6%; Score 329.2; DB 9; Length 349; 99.1%; Pred. No. 2.6e-69; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1737716"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Fax: 81-45-503-2216

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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
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                                                        On Jun 8, 2000 this sequence version replaced gi:8383516.
Contact: Yoshihide Hayashizaki
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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/strain="C57BL/6J"
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3']. CDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 626)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 ACGCTCGGCCTGCCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 GTGGCTGTCGGAAGCCTCAGGAAGCCCCGCAATGACCTGGGATACTCTGGGATC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 TGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCCAGGAAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGICCCCAGIGAAGGIGACAGCCCIGGGCGGIGGGAAGIIGGAAGCCACGIICACCIIC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 GITITCCCTGTGAGAATAATAGCTCTGGAAGGAGACTTGGAGACCACACAGTTGTATTC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 ATCAGGGAGGATCGCTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGGC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 IGGAACAAIGGTCAIIGCCGTGAGITIAAAIITCGTGAIGAAGAAAACAGAAGAGCTGGC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 AAATACAGCGCCTATGGGGGGAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGAC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 CACTACATCITITACTGCAAAGACCAGCACCATGGGGGCCTG---CTCCACATGGGAAAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426 CTTGTGGGTAGGAATTCTGATACCAACCGGAGGCCCTGGAAGAATTTAAGAATTGGTG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 CAGCGCAAGGGACTCTCGGAGGACGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTT 545
                                                                                                                                                                                                                                                                                                                                                                                                                     9 GTGACCTGCCGAGGTCGGCACCACAGAGCTCTGGAGATGAAGACCCTGTTCCTGGGTGTC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                         Score 171.2; DB 10; Length 603;
Pred. No. 4.6e-31;
0; Mismatches 238; Indels 4;
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                                                                                                                                                                        137 t
                                                                                                                                                                        167 g
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                                                                                                                                                                                                                                                                         Query Match 24.7%;
Best Local Similarity 58.3%;
Matches 338; Conservative
                                                                                                                                                                        131 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                        168 a
                                                                                                                                                                    BASE COUNT
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δ 셤 οy 셤 3;

Length 519; Indels

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Anote—"Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; ist strand CDNA was prepared from a modified polylinker; ist strand CDNA was prepared from prognant mouse uterus, and was then primed with a Not I and colloc(dT), primer. Double-stranded cDNA was ligated to Eco RI daptors (Pharmacia), dispersed with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized Library was constructed by Bento Soares and M. Fatina Bonalos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 bp mRNA linear EST 15-MAY-1995
T358 Rat incisor (noncalcified tissues) Rattus norvegicus cDNA
cione Y386 5' end similar to odorant-binding protein (RYSO12), mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 494)
Matsuki,Y., Nakashima,M., Amizuka,N., Warshawsky,H., Goltzman,D.,
Yamada,K.M. and Yamada,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 GAAGGAGACTTGGAGACCACAGTTGTATTCTGGAACAATGGTCATTGCCGTGAGTTTAAA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 ACCCTGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 GACTITICCGGAGGACAGGAGGCCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 ATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGCTC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 TTCGTGATGAAGAAAAGAGAAGAGCCTGGCAAATACACCGCTTTTCATAACACGAAGGTT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 ATGIACCIGCAGGAGCIGCCCAGGAGGGACCACIACAITIIACIGCAAAGACCAGCAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 CATGGGGGCCTG---CICCACAIGGGAAAGCITGTGGGTAGGAATTCTGATACCAACCGG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 AATGGGACGTCGTCATTCGGGATGGGAAAGCTCATGGGGAGAGACTCTGGTGAAAATCCA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 GAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGAAGGGACTCTCGGAGGACATT 515
                                                                                                                                                                                                                                                                                                                                                                                                                     39 CTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCTTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 CIGCICCICACCAICCIGCIGCIGCIGGIGGCIGCICAGAAGCCCCG 86
                                                                                                                                                                                                                                                                                                                               23.4%; Score 162.2; DB 9;
59.6%; Pred. No. 6.7e-29;
tive 0; Mismatches 194;
     /clone_lib="Soares_NMPu"
/sex="female"
                                             /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7029.1 GI:807371
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 59.6 Matches 291; Conservative
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mamalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 519)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unbublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Bmall: cgapbs-r@mall.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:918805
                                                                                                                                                                                                    246 GTGGAAAAGACGTCGGTGAATGAGCACTACATTTTCTACTGCGAAAAGCCGGCACAATGAGG 305
                                               Gaps
                                                                                     105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                                                                                                           165 CCGGAGGACAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG 224
                                                                                                                                                                                                                                                                   284
                                                                                                                                                                                                                                                                                                                                                   285 ATGCGGAAGACGGAGGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTAC 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 ACGICGICATICGGGAIGGGAAAGCICAIGGGGAGAGACICIGGIGAAAAICCAGAGGCC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 CTGGAAGAATITAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACG 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 ATGGAAGAATTTAAGAATTTCATAAAGGGCATGAATCTCCGACTGGAAAACATGTTTGTG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 CCCCIGCAGACGGGAAGCIGCGIICCCGAACACIAGGCAGC-CCCCGGGGICTGCACCICC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GACCTGGTGGATTACTCTGGGATCTGGTACGCAAAGGCCATGGTACAATGGTACCCTA 65
                                                                                                                                                                                                                                                                225 AAGTIGGAAGCCACGTICACCTICATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                      345 CTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGG
                                               4:
     DB 10; Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             581 AGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCTGGACCTACCCTC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 TGAGCCAGCCTTGCTTCCAACACCAAGCTGGGACATCCCTTCACCACCCCC 537
  Score 169.6; DB 10; Length
Pred. No. 1.1e-30;
0; Mismatches 209; Indels
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Seq primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 503.
Location/Qualifiers
1. 519
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1434737"
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A1877465.1 GI:5551514
  24.5%; 60.0%;
                      Best_Local Similarity 60.0
Matches 319; Conservative
                    Similarity
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Query Match
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AI877465
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Email: smith@email.marc.usda.gov
Sinjle pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMETS
                                                                                            Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidea; Bovinae; Bos.
1 (Dases 1 to 337)
                                                                                                                                                                      1 (bases 1 to 337)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Gass, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                      Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pcMv SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, thymus, senitendonous muscle, longissimus muscle, pancreas, adreal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 CCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGACCAGGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ICAICAGGGAGGAICGGIGCAICCAGAAGAAATCCIGAIGCGGAAGACGGAGGAGCTG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 gagagecegaagececadarardaaagecergerecreecearececreereagerreere 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GGCAGCACAGACCTCTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 148; DB 12; Length 337;
Pred. No. 1.6e-25;
0; Mismatches 85; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Usba Center, NE 68933-0166, USA
THEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 GCAAATACAGCGCCTATGGGGGCAGGAAGC 336
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Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9913"
/clone_lib="MARC 2BOV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
BF193883
BF193883,1 GI:11077252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.4%;
Best Local Similarity 68.8%;
; Matches 227; Conservative 0
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                                                                                    Bos taurus
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/clone_lib*Rat incisor (noncalcified tissues)*
/lab_host="Xx-1 blue"
/note="Vector: Bluescript II SK -; Site_1: Eco RI; Site_2:
Xno I; The apical portion and the entire pulp of the
maxillary and mandibular incisors from 3-4 week old rats
were excised. A cDNA library was constructed in the LRAP
II vector (Stratagene) by use of poly A+RNA from these
tissues. The phage cDNA library was converted into a
Bluescript phagemid cDNA library by in vivo excision by
the Exassist/Solm system (Stratagene).

15 a 101 c 144 g 96 t 8 others
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  of randomly selected cDNA clones
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                                                                                                        Laboratory of Developmental Biology, National Institute of Dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGCTCATGTACCTGCAGGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 GCTGCCCAGGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 CCTGTTCCTGGGTGTCACGCTCGGCCTGCCCTGTCCTTCACCCTGGAGGAGGA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 CAGGAGGCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 CCACATGGG-----AAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 ATCINAAGGGGGAAACICGIIGGGGAGGAICTINAGGACAACCCAGNGGGCCAIGGNG 448
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Pred. No. 1.7e-27;
0; Mismatches 184; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Building 30, Room 405, Bethesda, MD 20892
Tel: 301405111
Fax: 3014020897
Emmil: yammdd@yoda.nidr.nih.gov
Seg primer: AACAAAAGCTGGAGCTCCACC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/strain="Sprague-Dowley"
/db_xref="taxon:10116"
/clone="Y358"
  A compilation of partial sequences
from the rat incisor
                                       J. Dent: Res. 74, 307-312 (1995)
95181657
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                                                                                    Contact: Yamada Y
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us-09-099-823-4.rst

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Email: mESY@mil.inh.gov
The sequence contained an oligo-df track that was present in the
The sequence contained an oligo-df track that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NorI site
and the oligo-df track served to identify it as a clone from the
normalized olfactory buibs library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP CDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seg primer: MI3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 bp mRNA linear EST 18-SEP-1999 UI-M-BHI-amt-h-10-0-UI.SI NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-HHI-amt-h-10-0-UI.3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Soiurognathi; Muridae; Musinae; Mus.
I (basses I to 501)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
379 TITACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGA 438
                                        362 TCTACTATGAGGGCAAAATACACAGACATCATTTCCAAATTGCAAAACTCGTGGGCAGAA 421
                                                                                     439 ATTCTGATACCAACCGGGGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGAC 498
                                                                                                              499 TCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACATA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-amt-h-10-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spinal cord libraries.
TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE-olfactory-bulbs
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/organism="Mus_musculus"
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AW049121.1 GI:5909650
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Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                AW920286 EST 25-MAY-2000 SS4 bp mRNA linear EST 25-MAY-2000 EST351590 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIGT45 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissuc_type="mix - brain, ovary, placenta, kidney, lung, liver, embryo, heart, muscle, spleen"
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; Estimated insert size approx.1 kb"
153 c 148 g 124 t
                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                          Lee,N.E., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="Reficient"
/clone=lib="Fat gene index, normalized rat, norvegicus,
Bento Soares"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CCCAGGCCTTCCCCACCACGAAGAAATAGGATGTGTCAGGAACGTGGTATTTGAAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 CCAIGGIGGICGAIAAGGACIIICCGGAGGACAGGA---GGCCCAGGAAGGIGICCCCAG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 ATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGCGGAGGAGCCTGGCAAATACAGCG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GACGGTGCCAGGAGATGAGCACTGTCCTAGAGAGACAGGATGAACCTGGCAATACACAG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: (301)-838-552,
Fax: (301)-838-0208
Fax: (301)-883-0208
Famil: nhleeklyin.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Onpublished (1998)
Ontact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, 18
Fax: (301)-888-529
Fax: (301)-888-0208
                                                                                                                                                                  AW920286.1 GI:8086095
                                                                                                                                                                                                                                                                                                                           (bases 1 to 594)
                                                                                                                                                                                                               Norway rat.
Rattus norvegicus
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157 t TAG_SEQ-CATGG" 112 a 109 c 123 g BASE COUNT ORIGIN

;; Query Match 17.3%; Score 119.8; DB 10; Length 501; Best Local Similarity 60.1%; Pred. No. 1.2e-18; Matches 235; Conservative 0; Mismatches 152; Indels 4; Gaps δŏ

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483 GTGCAGCGCAAGGGACTCTCGGAGGACGACATTTTCACGCCCCTGCAGAGGGGAAGCTGC 542 g ŏ

g

602 CACAGAGCCGGACCAGCTGGACCTACCCTC 632 ŏ

Search completed: February 10, 2003, 04:58:23 Job time : 1928.58 secs

Mon Feb 10 11:12:02 2003

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

February 9, 2003, 22:02:40; Search time 2254.33 Seconds (without alignments) 8933.518 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-099-823-5 692 1 GAGGCCGAGTGACCTGCCGA.....ATAAAGTCCTTCTCCCCCCA 692 Title: Perfect score: Sequence: Scoring table:

2054640 segs, 14551402878 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

4109280

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

em_htgo_hum: * em_htgo_mus: * em_htgo_other: * ä

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

								SUMMARIES	
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PAT 06-JUL-2002

linear

DNA

ALIGNMENTS

Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS

Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.

PAT 16-AUG-2002

DNA

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Best Local Sim
Matches 690;
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and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 205 31-JAN-2002;
Generach, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
Generach, Inc. (US); Baker, Kevin P. (US); Genber, Hanspeter (US); Genter, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin I. (US);
Hillan, Kenneth J. (US); Marsters, Soch A. (US); Pan. James (US);
Pacani, Micholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
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RESULT 2 AX491098

ö Baker.K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.W., Wood,W.I. Ediaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 240 241 TCACCTTCAFGAGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGG 300 TGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGAAGCT 540 541 GCGTTCCCGAACACTAGGCAGCCCCCGGGGTCTGCACCTCCAGAGCCCACCCTACCACCAG 600 9 reserercacecresceresces at 120 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180 301 AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCA 360 GGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420 GAAAGCTIGIGGGIAGGAATICIGAIACCAACCGGGAGGCCCTGGAAGAAITTAAGAAAI 480 ACACAGAGCCCGGACCACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCC 660 Gabs 1 GACGCCCAGTGACCTGCCGAGGTCGGCACCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60 Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
Patent: WO 0200690-A 205 03-JAN-2002;
Genentech, Inc. (US)
Location/Qualifiers 1 GACGCCCCAGTGACCTGCCGAGGTCGGCCAGAGCTCTGGGAGAGATGAAGACCTGTCC 181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT ö 99.5%; Score 688.8; DB 6; Length 739; llarity 99.7%; Pred. No. 7.2e-146; Conservative 0; Mismatches 2; Indels 0; AX491098 739 bp 1 Sequence 205 from Patent WO0200690. 117 /organism="Homo sapiens" /db_xref="taxon:9606" 1 207 c 205 g 117 AX491098 AX491098.1 GI:22323886 Homo sapiens Similarity 210 a and Ye, W. human. 601 쉱

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/translation="MKTLFLGVPLGLAAALSFTLEEDITGTWYKAAVVDKDPBDR
PREVSPWYDWYGGGELLEAFPREDREDRYCKFLLARKTEEDFGKFASYGGKLEATUTLO
RIPROBITTYTCKDQHGGLLAHGKLVGRNSDYNREALGEFKKLVQRKGLSEBEITTP
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1. (Dases 1 to 676)
Lacazette, E., Gachon, M. and Pitiot, G.
A novel thuman odorant-binding protein gene family resulting from genomic duplicons at 9q34. differential expression in the oral and gental spheres
Hum. Mol. Genet. 9 (2), 289-301 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSA251026 676 bp mRNA linear PRI 02-FEB-2000
Homo sapiens mRNA for putative odorant binding protein b-a (OBFILD
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2 (bases 1 to 676)
Gachon, A.M.
Direct Submission
Submitted (26-007-1999) Laboratoire de Biochimie Medicale - INSERM U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri Dunant, Clermont Ferrand cedex01 63001, FRANCE Location/Qualifiers
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                                                                                                   540
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                                                                                                                                                                              421 AAGCTICIGGGIAGGAATICIGAIACCAACCGGGAGGCCCTGGAAGAAITIAAGAAAIIG 480
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                                                                              483 GIGCAGCGCAAGGGACTCTCGGAGGAGACATTTTCACGCCCCTGCAGACGGGAAGCTGC
                                                                                                                                                       543 GITCCCGAACACTAGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACAGAC
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/db_xref="G1:6900077"
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47251026.
47251026.1 GI:6900076.
60BTID gene; odorant binding protein.
ROmo sapiens.
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/organism="Bomo sapiens"

/db_xref="taxon:9606"

/cbromosome="9"

/map="934"

43. .555

/gene="OBPIID"
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CTGACTCCAAATAAAG 676
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/db_xref="GI:13185355"
/db_xref="GI:13185355"
/tb_xref="GI:13185355"
/tb_xref="GI:1318555"
/tb
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pitlof.6., Lacazette,E. and Gachon,F.
Odorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polymucleotides coding for said polypeptides and
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/note="cDNA2098 (676) - forme classique (hOBPIIb-alpha)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTC 242
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uses thereof
Patent: WO 0112806-A 9 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
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1. .67--, xwalliers
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/db_xref="taxon:9606"
43. .555.
     AX083544 676 bp
Sequence 9 from Patent W00112806.
AX083544 AX08354.1 GI:13185354
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/translation="MKTLETLGYTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDR
RPRAVSFWKYTALGGGNLEATFTEMREDRCIQKKILMRKTEEPGRFSAYGGRKLITLQ
ELPGYDVYFYCKDQRRGGLRYMGKLVGRNPNTNLEALEEFKKLVQHKGLSEEDIFMP
LOTGGSCYLEH" 204 g 115 t
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
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                                                                                                                                                                                                                                                                                        423 AAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTG 482
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                                                                                                 Query Match 93.8%; Score 648.8; DB 6; Length 676; Best Local Similarity 97.5%; Pred. No. 8.3e-137; Matches 659; Conservative 0; Mismatches 17; Indels 0
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A7251021.
A7251021.1 GI:6900066
OBFIIa gene; odorant binding protein.
Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 676)
Pitiot, G., Lacazette, E. and Gachon, F.
Podovant-binding human proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and
uses thereof
                                61 GGTGTCACGCTCGGCCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 120
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                                                                         GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCC
                                                                                         GGGACCTGGTAGGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCC
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Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 676
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Sequence 1 from Patent W00112806.
AX083536 AX083536.1 GI:13185346
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Universite of Autorgane (PR); Pitiot, Gilles (FR)

Universite of Autorgane (PR); Pitiot, Gilles (FR)

Location/Qualifiers

1...604

Ab_ratef="taxon:9606"

Ab_ratef="taxon:9606"

Ab_ratef="charatel"

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                                                                                                                   241 ACCTTCATGAGGGAGGAGGATCGGTGCATCCAGAAAATCCTGATGCGGAAGACGGAGGG 300
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                                                 85.2%; Score 589.8; DB 6; Length 725; 90.9%; Pred. No. 2e-123; Live 0; Mismatches 17; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Sequence 3 from Patent W00112806.
AX083538.1 GI:13185348
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2 (Dasses 1 to 676)

Gachon,A.M.

Submitted Submission

Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INNERM

U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri

Dunant, Clermont Ferrand cedex01 63001, FRANCE
Lacazette, E., Gachon, A.M. and Pitiot, G. A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
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Num. Mol. Genet. 9 (2), 289-301 (2000)
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linear PAT 28-FEB-2001
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 AGGAAGGIGICCCCAGIGAAGGIGACAACCCIGGGCGGIGGGAAGIIGGAAGCCACGIIC 242
                                                                                                                                                                                                                                                                                                                                 243 ACCITCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGAGGGGGG 302
                                                                                                                                                                                                                                                                                                                                                                                        303 CCTGGCAAATACAGCGCCTATGGGGGCCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGG 362
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                                                                                                                                                                  GGTGTCACGCTCGGCCTGGCCGCTGCCTTCACCCTGGAGGAGGAGGATATCACA 122
                                                                                                                                                                                                                       123 GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCC 182
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                                                                                                            3 CGCCCAGTGACCTGCCGAGGTCGGCACACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62
                                                                                                                            49;
                                                    85.2%; Score 589.8; DB 9; Length 725; illarity 90.9%; Pred. No. 2e-123; Conservative 0; Mismatches 17; Indels 49;
ELPGTDDYVFYCKDQRRGGLRYMGKLVGPCRCPHVGSPGHLTCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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Sequence 5 from Patent WO0112806.
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AX083540.1 GI:13185350
                                                                      Best Local Similarity
Matches 659; Conserv
              163 a
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TAAAG 725
                                                       Query Match
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AX083540
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KEYWORDS
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RPRKVSPVXVTALGGGNLEAFFFREDRCIQKKILMRKTEEFGKFSAYGGRKLIYLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Frimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
Lacazette, E., Gachon, A.M. and Pitiot, G.
A novel human odocrant-binding protein gene family resulting from genomic duplicons at 9q34; differential expression in the oral and genomic duplicons at 9q34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (26-027-1999) Laboratoire de Biochimie Medicale - INSERM
Submitted (26-027-1999) Laboratoire de Medecine, 28, place Henri
Dinat, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
1. 725
(db.ref="textor") 1. 675
(db.ref="textor") 19606"
                                               301 CCTGGCAAATTCAGCGCCTATGGGGGCAGGAAGCTCATATACCTGCAGGAGCTGCCGGG 360
                              363 AGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGA 422
                                                                                    494 GGGACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACA 553
                                                                                                                                                                                                             554 CTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGAGACACAGAGCCCGG 613
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OBPTIA gene; odorant binding protein.
Homo sapiens
Homo sapiens
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/gene="OBPIIa"
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2 (bases 1 to 725)
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| 721 TAAAG 725
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KEYWORDS
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HSA251022
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/product-"putative odorant binding protein ag"

protein_id="CABN131:1"
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REPGYPOYPTCKDORGGLRYMGKLYNSAPCRAYPLSPRRLYWPPHLQVGILIFTWR
PWKNLRNWGSTRDSRRRYFSCPRCRRAARSWYRQPPGLLLGFWR

                                                                                                                                                               HSA251024 741 bp mRNA linear PRI 02-FEB-2000 Homo sapiens mRNA for putative odorant binding protein ag (OBFIIA
                                                                                                                                                                                                                                                                                                                                                                   Lecasette, E., Gachon, A.M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from genomic duplicons at 9934: differential expression in the oral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Direct Submission
Submitted (26-00T-1999) Laboratoire de Biochimie Medicale - INSERM Submitted (26-00T-1999) Laboratore - Faculte de Medecine, 28, place Henri Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 741)
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661 CAGACACAGAGCCCGGACCACCTGGACCTACCTCCAGCCATGACCCTTCCCTGCTCCCA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTCGCAGGAGGAGGATATCACA 122
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88.9%; Pred. No. 8.3e-120;
tive 0; Mismatches 17; Indels 65.
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Hum. Mol. Genet. 9 (2), 289-301 (2000)
20076326
                                                                                                                                                                                                          gene).
AJZ51024.1 GT:6900072
OBPIIa gene; odorant binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xeef="taxon:9606"
/chromosome="9"
/map="9434"
43, .729
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                                    658 CCCACCIGACICCAAAIAAAG 678
                                                           721 CCCACCTGACTCCAAATAAAG 741
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Gachon, A.M.
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229 c
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Matches 659; Conservative
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Homo sapiens
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ORIGIN
                                                                                                                                                                                    DEFINITION
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VERSION
KEYWORDS
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HSA251024
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/codon_start=1
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PWIKNLRNWGSTRDFSCPCRREAAFSNTROPPGSPHILDTPR
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                 odorant-binding human processing fixing hydrophobic ligands: polypeptides and polynucleotides coding for said polypeptides and uses thereof
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Pred. No. 8.3e-120;
0; Mismatches 17; Indels 65;
                                                                                             Universite d'Auvergne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. .741
    Pitiot, G., Lacazette, E. and Gachon, F.
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                                                                        Patent: WO 0112806-A 5 22-FEB-2001;
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43. .729
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Best Local Similarity 88.9%;
Matches 659; Conservative
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HSA251027 782 bp mRNA linear PRI 02-FEB-2000 Homo sapiens mRNA for putative odorant binding protein bb (OBPLIb
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                 61 GETGTCACGCTCGGCCCTGCCCTGTCTTCACCCTGGAGGAGGAGGATATCACA 120
                                                                                                                                                                                                                                                                                                                                         GGGACCIGGIACGIGAAGGCCATGGIGGICGATAAGGACTITICCGGAGGACAGGAGGCCC 182
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                                                               3 CGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG
                                                                                                                                                                                                                  303 CCTGGCAAATACAGCGCCT--------
                               Indels 106;
Length 782;
Query Match 80.9%; Score 560; DB 6; La
Best Local Similarity 86.4%; Pred. No. 1.1e-116;
Matches 676; Conservative 0; Mismatches 0;
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AJ251027.1 GI:6900078
OBFILD gene; odorant binding protein.
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Buxaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 782)
Pitiot, G., Lacazette, E. and Gachon, F.
Polypeptides and polynucleotides coding for said polypeptides and polynucleotides coding for said polypeptides and sees thereof
                               243 ACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAG 302
                                                               241 ACCTTCATGAGGGAGGATCGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAG 300
                                                                                                303 CCTGGCAAATACAGCGCCTATGGGGGCCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGG 362
                                                                                                                     363 AGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGA 422
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                                                                                                                                                                                                                                                                                                           Patent: WO 0112806-A 11 22-FEB-2001;
Universite d'Auveragne (FR); Pitiot, Gilles (FR)
Location/Qualifiers
1. 782
/Organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 11 from Patent W00112806.
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GAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG 496
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481 CITITACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAG 540
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                                                                      497 ACTCTCGGAGGAGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTA
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illarity 99.8%; Pred. No. 2.4e-106;
Conservative 0; Mismatches 1;
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Conklin,D.C.
Antibodies to lipocalin homologs
Patent: US 6365716-A 1 02-APR-2002;
Location/Qualifiers
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AR204078 AR204078.1 GI:21500632
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     1 (bases 1 to 782)
Lacazette, E., Gachon, A.M. and Pitlot, G.
A novel human odcrant-binding protein gene family resulting from
genomic duplicons at 9934; differential expression in the oral and
                                                                                                                                                                                                                                  Direct Submission
Submitted (26-00T-1999) Laboratoire de Biochimie Medicale - INSERM
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex01 63001, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GETGTCACGCTCGGCCTGGCCGCTGTCCTTCACCCTGGAGGAGGAGGAGATATCACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTC 240
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Hum. Mol. Genet. 9 (2), 289-301 (2000)
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/gene="OBPIIb"
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Db 362 CATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAG 421 Qy 459 GCCCTGGAAGAATTTAAGAAATTGGTGCAGGGAAGGACTCTCGGAGGAGGACATTTC 518		REFERENCE 1 (Dasses 1 to 542) AUTHORS Pitiot, G., Lacazette, E. and Gachon, F. TITLE Odorant-binding human proteins fixing hydrophobic ligands: POLYpeptides and polynucleotides coding for said polypeptides and uses thereof and polynucleotides coding for said polypeptides and DOURNAL Patent: WO 0112806-A 13 22-FEB-2001; Universite d'Auvergne (FR); Pitiot, Gilles (FR) FEATURES FOURCE 1. 542	/Organism="famo sapiens" (db_raref="taxon:9606" 43300	Ouery Match 61.7%; Score 426.8; DB 6; Length 542; Best Local Similarity 99.5%; Pred. No. 1.7e-86; Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 249 AIRAGGAGGAGATCAGAAAAAACCGAAGAAGACGAAGACCTGGC 308	Db 113 41GAGGGAGGGCTCCGGAGGAAAATCTGGAGGGAGGGCCTGGC 172	QY 369 CACTACATCTTTACTGCAAGACCAGCACCATGGGGGCCTGCTCCACATGGGGAAGCTT 4.28	QY 489 GGCAAGGGACTCTGGGAGGACATTTCACGCCCTGCAGAACGGGAAGCTGCC 548	609
Db 361 CATGGGGGCCTCCACATGGGAAAGCTTGTGGGTAAGAATTCTGATACCAACCGGGAG 420 Qy 459 GCCTGGAAGAATTAAGAAATTGGTGCAGCCAAGGGCTCTCGGAGGAGACATTTC 518 [AX451327 LOCUS AX451327 LOCUS AX451327 AX451327 AX451327 AX451327 AX451327 AX451327 AX45137 AX	AUTHORS LOK, S., Foster, D.C. and Holloway, J.L. TITLE Use of human phermone polypeptides JOURNAL Patent: WO 0223201-A 1 21-MAR-2002; ZymoGenetics, Inc. (US) FEATURES SOURCE 153 ACTOR LOCATION QUalifiers SOURCE ACTOR LOCATION GRAPHENS ACTOR LOCATION SAPIens ACTOR LOCATION	NT 125 a	Query Match 74.3%; Score 514.4; DB 6; Length 523; Best Local Similarity 99.8%; Pred. No. 2.4e-106; Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 39 CTGGGARAGACCCGGGGGGGGGGGGGGGGGGGGGGGGCGGGC	DD	QY 159 GACTITCCGGAGGACAGGACGCCAGGAAGGTGCCCAGTGAAGGTGACAGCCCTGGGC 218 Intititititititititititititititititititi	QY 279 ATCCTGATGCGGAAGAGCGGCAAATACAGCGCCTATGGGGGCAGGAAGCTC 338 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	

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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
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score greater than or equal to the score of the result being printed,
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                      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Database :

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                                BS124; breast; cancer; detection; diagnosis; prevention; treatment; consensus; EST; ss.
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                                                                                                                                                                                                                                                                     Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;
Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a consensus BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 692;
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 Human BS124 specific EST clone consensus sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 95; 125pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
                                                                                                               WO9859049-A1.
                                                                                                                                                                             19-JUN-1998;
                                                                                  Homo sapiens.
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                                                                                                                                                                                      100.0%; Score 692; DB 20; Length 692; llarity 100.0%; Pred. No. 4.2e-168; Conservative 0; Mismatches 0; Indels 0
                                                                       The sequence is that of a BS124-specific EST clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                       Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;
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Best Local Simi
Matches 692;
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99US-0144758
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30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relatest to methods for diagnosing, monitoring, staging, inaging and treating breast cancer (BC). The methods comprise measuring the levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelied and used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
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                                                                                                                                                                                                                                 Query Match 99.7%; Score 690; DB 21; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.4e-167;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGCCCAGTGACCTGCCGAGGTCGGCACACACACTCTGGAGATGAAGACCCTGTTCC 60
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      541 GCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ91770 standard; DNA; 690 BP
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Best Local Si
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breast
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Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antiheumatic; immunosuppressive; haemostatic; antiarthritic; antiheumatic; immunosuppressive; antiandemic; hepatotropic; antidiabetic; antiallargic; antiandemic; hepatotropic; virucide; antipacriatic; antiallargic; antiantamic; systemic lugus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; didopathic inflammatory myopathy; systemic sclerosis; sarcoidosis; systemic vasculitis; autoimmune haemolytic aneemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; unune-mediated six, whipple's disease; intialmmatory bowel disease; gluten-sensitive enteropathy; unfolmmune disease; immune-mediated skih disease; allergic disease; munue-mediated skih disease; allergic disease; agraft rejection; graft-versus-host-disease; ss.
                                                                                                                                                                                                                                                                                                                                Human PRO1283 protein UNQ653 encoding cDNA SEQ ID NO:169.
                                                        661 ACCTGACTCCAAATAAAGTCCTTTTCCCCCAA 692
                          661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
                                                                                                                                                                                         AAC58615 standard; cDNA; 739 BP
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99US-0123957.
99US-0125775.
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99US-0162506.
99WO-US28214.
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99US-0131445
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99WO-US12252
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99US-0146222
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30-NOV-1999;
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06-JAN-2000;
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                                                                                                                                                                                                                                     AAC58615;
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ACC 58 6115
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                                                                                                                                                                                                                               Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
                                                                           Fong S;
Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or Knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGGGTGTCACGCTCGCCTGCCCTGCCTCCTTCCTTCCTCCTGGAGGAGGAGGAGGATTCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGAGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 TGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 GCGTTCCCGAACACTAGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 ACACAGAGCCCGGACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACGCCCAGTGACCTGCCGAGGTCGGCACACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGGAAGTTGGAAGCCACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onery March 99.5%; Score 688.8; DB 22; Length 738; Best Local Similarity 99.7%; Pred. No. 2.8e-167; Marches 690; Conservative 0; Mismatches 2; Indels 0;
                                                                Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Goddard A, Goddowski PJ, Grimaldi CJ, Gurney AL, Pan J, Faoni NF, Roy MA, Smith V, Stewart TA, Tumas D; Watanabe CK, Williams PM, Wood WI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 738 BP; 209 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 99; 787pp; English.
                        (GETH ) GENENTECH INC.
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541 GCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAG 600
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                                                                                                                                                                                                                                                                                   Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
      361 GGAGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG
                                          GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAT
                                                                                                                                    481 TGGTGCAGCGCAAGGGACTCTCGGAGGACGACATTTTCACGCCCCTGCAGACGGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO1283 (UNQ653) cDNA sequence SEQ ID NO:161.
                                                                                                                                                                                                                                                                                                                                   661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
                                                                                                                                                                                                                                                                                                                                                      661 ACCIGACTCCAAATAAAGICCITTTCCCCCAA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA37071 standard; cDNA; 739 BP.
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9805-0098843.
9805-0099536.
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9805-0099598.
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9803-0099803.
9803-0099812.
9803-0099815.
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98US-0100662.
98US-0100664.
98US-0100683.
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10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
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10-SEP-1998;
10-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                              The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, caletocal from systemic lupus erythematosus, rheumatoid arthritis, systemic selected from systemic lupus erythematory myopathies, Sjogran's systemic vascullitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thromboytopeenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central bowel disease, glutten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic disease, autoimmune or immune-mediated skin diseases, allergic disease, autoimmung graft respection and graft-versus-host-disease. AACSB378 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences AACSB372 and AABB3414 to AABB3417 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                           Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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                                                                                                                                               Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTTCCGGAGGACAGGGGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  Claim 23; Fig 73; 309pp; English.
06-JAN-2000; 2000MO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000MO-US04414.
                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                      WPI; 2000-572271/53.
P-PSDB; AAB33450.
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New mammalian DNA sequences encoding transmembrane, receptor or secreted PNO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO Polypetides given in AAY99480 to AAX99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TGGGTGTCACGCTCGGCCTGGCCGCTGTCCTTCACCCTGGAGGAGGAGGAGGATATCA 120
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                                                                                                                                                                                                                                                                                                                            Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%; Score 688.8; DB 21; Length 739; 99.7%; Pred. No. 2.9e-167; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                            Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                           Smith V,
                                                                                                                                                                                                                                                                                                                            Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 99; 773pp; English.
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Best Local Similarity 99.79
Matches 690; Conservative
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P-PSDB; AAY99389.
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, anging, myocardial infarctions, thromophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams FM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TGGGTGTCACGCTCGGCCTGGCCGCTCCTCTCACCTGGAGGAGGAGATATCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;
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                                                                                                                                                                                                     2001US-0866034.
2001WO-US17092.
2001US-0870574.
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2001WO-US19692.
2001WO-US000000.
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(GERK) GERRITSER M.
(GODD) GODDARD A.
(GODD) GODDARD A.
(HILLA HILLAN K J.
(HARS) MARSTERS S.
(PANJ) PAN J.
(PANJ) PAN J.
(RARS) MARSTERS S.
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FERRARA N.
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                                                                                                                     420
                                                                                                                                                                                                                481 TGGTGCAGCGCAAGGGACTCTCGGAGGACAATTTTCACGCCCCTGCAACACGACGAAGCT 540
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                                                                                                                                                                                421 GAAAGCITGIGGGIAGGAATICIGATACCAACCGGGAGGCCCIGGAAGAAITTAAGAAAI 480
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                                                                                          Human angiogenesis related cDNA PRO1283 SEQ ID NO: 205.
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2000US-220624P.
2000US-220664P.
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08-NOV-2000;
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28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
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24-AUG-2000;
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                                              241 TCACCTTCATGAGGGAGGATCGGTGCATCCAGAAAATCCTGATGCGGAAGACGGAGG 300
                                                                                                                                   601 ACACAGAGCCGGGACCACCTGGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCC 660
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                                                                                                                      361 GGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420
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Human PRO1283 cDNA sequence SEQ ID NO:205.
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2000WO-US23328.
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25-JUL-2000;
28-JUL-2000;
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24-AUG-2000;
07-SEP-2000;
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17-AUG-2000;
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20-JUL-2000;
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ABB88072 to ABL88258 encode the PRO proteins given in ABB84817 to CC ABB85003. The PRO proteins and polymucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antianteriosclerotic.

CC activities, and can be used in gene therapy. The PRO polymucleotides, proteins, agonists and antaquists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, co-c. e.g. cardioratcopy, trauma, cancer, ge-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, corpumphagitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma and mound healing. The PRO polymucleotides have applications of in molecular biology, including use as Abbridistation probes, and in chromesome and gene mapping ABL88259 to ABL88254 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 regerercecceccecceccecceccecrerers 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoni NF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
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2001US-0854280.
2001US-0866028.
2001US-0866034.
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2001US-0870574
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2001WO-US17800
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P-PSDB; ABB84919.
08-NOV-2000; 2
10-NOV-2000; 2
10-DEC-2000; 2
20-DEC-2000; 2
22-JAN-2001; 2
28-FEB-2001; 2
09-MAR-2001; 2
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10-MAY-2001;
25-MAY-2001;
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05-APR-2001;
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243 ACCIICAIGAGGGAGGAICGGIGCAICCAGAAGAAAICCIGAIGCGGAAGACGGAGGAG 302
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                                                                                                                                           481 TGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCT 540
                                                                                                                                                                                          241 TCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGG 300
                                                  301 AGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCA 360
                                                                                   GGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGG 420
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44.2.55
//ttg= //product= "odorant binding polypeptide OBPLIb-alpha"
       181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGT
                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of odorant binding polypeptide OBPIIb-alpha.
                                                                                                                                                                                                                                                                                              661 ACCTGACTCCAAATAAAGTCCTTTTCCCCCAA 692
                                                                                                                                                                                                                                                                                    661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPID-alpha. OBPS provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc.. OBP polypeptides are used as binding proteins for Aptrophobic ligands (particularly odorants); as competitive inhibitors (squainsts or antagonists) of cellular lipocalcin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially concants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; for treating hyperlipidemia or obesity, or to supplement non-maternal cull when combined with nutritional farty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or foeto-placental pathology (rupture of the amniotic membrane); and as antiallergic agents.
New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 122
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Matches 676; Conservative 0; Mismatches
                                                                                                                                                                                  Disclosure; Page 113-114; 132pp; French
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GEGCAGCGCAAGGGACTCTCGGAGGAGACATTTTCACGCCCCTGCAGACGGAAGCTGC 540

GIGCAGCGCAAGGGACTCICGGAGGAGGACATTITCACGCCCCTGCAGGAGGGAAGCTGC 542

GTTCCCGBACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGAC 602

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Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia, obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
                                                                                                                                                                                                                                                    61 GERGICACGCTCGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 120
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/product= "odorant binding polypeptide OBPIIa-beta"
                                                                                                                                         183 AGGAAGGTGTCCCCAGTGAAGGTGACACCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of odorant binding polypeptide OBPIIa-beta.
   22; Length 676;
                                                      17; Indels
93.8%; Score 648.8; DB 2:
97.5%; Pred. No. 5.2e-157.
tive 0; Mismatches 17.
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43..483
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      Query Match
Best Local Similarity 97.55
Matches 659; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma, cancer; perfume; hyperligidenia; obseity; food additive; anticancer; foetus detexification; pregnancy marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
/*tag= a
/product= "odorant binding polypeptide OBPIIa-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of odorant binding polypeptide OBPIIa-alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 106-107; 132pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                               AAF80039 standard; cDNA; 676 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                          663 CTGACTCCAAATAAAG 678
                                                                                                                                         (UYAU-) UNIV AUVERGNE. (PITI/) PITIOF G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-202864/20.
P-PSDB; AAB67738.
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Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes -
                                                                                                                                           494 GGGACTCTCGGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACA 553
                                                                                                                                                                                                                                                     614 ACCACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCTGACTCCAAA 673
                                                                                                                                                                                                                                                                                                                                                                                                                 423 AAGCITGTG------GG 433
                                                                                                     421 AAGCTTGTGGGGGCCGTGCCGCTGTCCCCACGTCGGCTCACCTGGCCACCTCACCTGCAGG 480
                                                                                                                                                                                                                                                                                                           554 CTAGGCAGCCCCGGGGTCTGCACCTCCAGGCCCACCCTACCAGCACAGACACAGAGCCCGG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "odorant binding polypeptide OBPIIa-gamma"
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43..729
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(PIII/) PITIOT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-202864/20.
P-PSDB; AAB67740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 TAAAG 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AGGAAGGIGTCCCCAGTGAAGGIGACAGCCCTGGGCGGGGGAAGTIGGAAGCCACGTIC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 CCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 AGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGCCCAGTGACCTGCCGAGGTCGGCACACAGAGCTCTGGAGATGAAGACCTGTTCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CGCCCAGTGACCTGCCGAGGTCGCCACCACACACACCTCTGGAGATGAAGACCCTGTTCCTG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.2%; Score 589.8; DB 22; Length 725; 90.9%; Pred. No. 7.7e-142; Ive 0; Mismatches 17; Indels 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 108-109; 132pp; French.
                                                                                                                                                                                                                                                          Gachon F;
                                                                                                            11-AUG-2000; 2000WO-FR02319.
                                                                                                                                                    12-AUG-1999; 99FR-0010439
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Matches 659; Conservative
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                                                                                                                                                                                            (UYAU-) UNIV AUVERGNE. (PITI/) PITIOT G.
                                                                                                                                                                                                                                                                                               WPI; 2001-202864/20.
P-PSDB; AAB67739.
                                                                                                                                                                                                                                                                                                                                                                                                     release of perfumes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiallergic agents.
                            WO200112806-A2.
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release) of lipophilic compounds, so prolong the 'hold' of perfumes, considerate stc.. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect controlling volatilisation of an odorant, specifically in perfumes, cosmetics or distinfectant compositions; to screen compounds, especially conntrolling volatilisation of an odorant, specifically in perfumes, cosmetics or distinfectant compositions; to screen compounds, especially controlling volatilisation of selections; to supplement non-maternal analysis of complex perfume mixtures; to solubilise lipophilic compounds; for treating hyperlipidemia or obesity, or to supplement non-maternal control compounds and with mutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier content pathology (rupture of the amnibitic membrane); and as antiallergic agents.

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Sequence 741 BP; 165 A; 229 C; 220 G; 127 T; 0 other;

82.9%; Score 573.8; DB 22; Length 741; 88.9%; Pred. No. 1e-137; ive 0; Mismatches 17; Indels 65; Gaps 63 GGTGTCACGCTCGCCTGCCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 122 61 GGTGTCACGCTCGGCCTGGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 120 123 GGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCC 182 183 AGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGAAGTTGGAAGCCACGTTC 242 243 ACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAG 302 CCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGG 362 363 AGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGA 422 423 AAGCTTGTG------ 431 AATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAA 537 538 GCIGCGIICCCGAACACIAGGCAGCCCCCGGGICIGCACCICCAGAGCCCACCCIACCAC 597 598 CAGACACAGAGCCGGGACCACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCA 657 3 CGCCCAGTGACCTGCCGAGGTCGGCACCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62 -------GGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGA 477 Best Local Similarity 88.9 Matches 659; Conservative Query Match 303 132 셤 QΣ å ద 셤 g ζ ð ద ð 셤 δ δ 셤 δŽ 셤 g g 셤 ŏ ð ğ

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The invention relates to isolated polynucleotide (I) and purpertied (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome of gene mapping, and in recombinant production of (II). The polymetides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (I) is useful in gene therapy techniques (I). (II) is useful in gene therapy techniques (I). (II) is useful in gene therapy techniques (I). (II) is useful in gene therapy techniques (II). (II) and its binding partners are useful in medical and food supplement. (II) and its binding partners are useful in medical inapping of sites expressing (II). (I) and (II) are useful in reating (II) chartification of insological activity. The polypeptide and polynucleotide sequences have applications in the printed and to produce other types of deta and products dependent on DNA and diagnostic coding sequences of the invention.

Consideration, but was obtained in electronic format directly from Wipo at the printed the theorem in the printed at the pain the printed at the pain in the printed at the printed
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                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onery Match 82.3%; Score 569.2; DB 23; Length 603; Best Local Similarity 96.5%; Pred. No. 1.4e-136; Matches 600; Conservative 0; Mismatches 3; Indels 19;
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                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #11858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 11858; 103pp; English.
721 CCCACCTGACTCCAAATAAAG 741
                                                                                                                                    AAS76054 standard; cDNA; 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                          13-FEB-2002 (first entry)
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P-PSDB; ABG11867.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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AAS76054
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437 GAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG 496
Pitiot G, Lacazette E,
                     WPI; 2001-202864/20.
P-PSDB; AAB67743.
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                                                                                                            585 CCCACCTACCACCAGACACAGAGCCGGACCACCTGGACCTACCCTCCAGCCATGACCC 644
             61 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTGGTGGTAAGGACTTT 120
                                                                      180
                                                                                                284
                                                                                                                                                285 ATGCGGAAGACGCAGGAGGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGCTCATGTAC 344
                                                                                                                                                               241 ATGCGGAAGACGGAGGCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGCTCATGTAC 300
                                                                                                                                                                                                                 CIGCAGACGGGAAGCIGCGIICCCGAACACIAGGCAGCCCCCCGGGICIGCACCICCAGAG 584
                                                                                                                                                                                                                                                                                                                                                                  345 CIGCAGGAGCIGCCCAGGAGGACCACTACATCTITTACTGCAAAGACCAGCACCATGGG 404
                                                                                                                                                                                                                                                   405 GGCCTGCTCCACAIGGGAAAGCTTGTGGGTAGGAATTCTGAIACCAACCGGGAGGCCCTG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "odorant binding polypeptide OBPIIb-beta"
                                                            105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTT
                                               165 CCGGAGGACAGGAGGCCCCAGGAAGGTGTCCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG
                                                                                               225 AAGTTGGAAGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTG
                                                                                                                                                                                                                                                                                                    465 GAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of odorant binding polypeptide OBPIIb-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582 Trccrecrecrecres 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF80044 standard; cDNA; 782 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   645 Trecergereceaectea 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2000; 2000WO-FR02319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200112806-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-2001
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AAF80044
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The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPID-beta (long form). OBPs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of cradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc.. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly doctants); as competitive compositions or anisation of an odorants, psecifically respectives, to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, comments or disinfectant compositions; to screen compounds, especially docarants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; for treating hyperlipidemia or obesity, or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as a controlling calculation of the foetual; as a marker of pregnancy or closto-placemtal pathology (rupture of the amniotic membrane); and as antiallergic agents.
New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGTGTCACGCTCGGCCCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 GGGACCIGGIACGIGAAGGCCAIGGIGGICGAIAAGGACITICCGGAGGACAGGAGGCCC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 corgectataracaccecerectrecrectecacarecaccacateaccecerecte 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 CTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 cecceargeacereceasercescascasascreresasastreaasascererere 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ... 3 CGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 AGGAAGGIGICCCCCAGTGAAGGIGACAGCCCTGGGCGGTGGGAAGTIGGAAGCCCACGTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ACCITCAIGAGGAGGAICGGIGCAICCAGAAGAAAICCIGAIGCGGAAGACGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 CCTGGCAAATACAGCGCCT-----303 CCTGGCAAATACAGCGCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Opery Match 80.9%; Score 560; DB 22; Length 782; Best Local Similarity 86.4%; Pred. No. 3.6e-134; Matches 676; Conservative 0; Mismatches 0; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 782 BP; 186 A; 226 C; 239 G; 131 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322
                                                                                                                                                                Claim 6; Page 115-116; 132pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAK7937-AAK9303) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruman, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine, peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                 900
                                                556
                                                              GGCAGCCCCCGGGTCTGCACCTCCAGAGCCCTACCTACCACCAGACACAGAGCCCGGACC 616
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ACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao I Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1381-1382; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polynucleotide SEQ ID NO 360.
                                                                                                                                                                                                                                                                                                                                         AAK51815 standard; cDNA; 781 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2000; 2000015-0560975.
20-UNA-2000; 2000015-0596075.
19-JUL-2000; 2000015-05620325.
01-SEP-2000; 2000015-0654936.
15-SEP-2000; 2000015-0653561.
20-CCT-2000; 2000015-0593125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000;
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| AG 782
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                                                                                                                                                                                                                                 677 AG 678
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Zhao QA,
Xue AJ, Y
                                                                                                                                                                                                                                                                                                                                                                         AAK51815;
                                                                                                                                                                                                                                                                                                          RESULT 15
AAK51815
                                              497
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activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                              Note: Records for SEQ ID NO 2110 (AAX52581), 2111 (AAX52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                             71 GGTCGGCAGCACAAGAGCTCTGGAGAGAGCCTGTTCCTGGGTGTCACGCTCGGCCTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 GCCATGGTGGTCGATAAGGACTTTCCGGAGGACAAGGCCCAGGAAGGTGTCCCCAGTG 200
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                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 CCCTGCAGGCCGTGCCGCTGTCCCCACGTCGGCTCACCTGGCCACCTCACCTGCAGGTA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 GGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGG 495
                                                                                                                                                                                                                                                                                                                                                   21 GGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 CGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 GACTOTOGGAGGAGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556 AGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCTACCACCAGACACAGAGCCCGGAC
                                                                                                                                                                                                                                               Query Match 78.6%; Score 543.8; DB 22; Length 781; Best Local Similarity 88.5%; Pred. No. 5.2e-130; Matches 629; Conservative 0; Mismatches 17; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 781 BP; 172 A; 234 C; 233 G; 142 T; 0 other;
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completed: February 9, 2003, 22:02:28 le : 259.241 secs

Scoring table: Perfect score:

Database

Sequence:

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                                                                                                                       GACTTTCCGGAGGACAGGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACACACCCTGGGC
                            sequence seq
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Pred. No. 1.1e-125;
0; Mismatches 1; Indels 0;
US-09-130-663-13

US-09-614-022-13

US-09-614-702-13

US-09-244-796-17

US-09-130-663-23

US-09-130-663-23

US-08-182-175A-56

US-08-182-175A-56

US-08-182-177A-74

PCT-US92-06412-56

US-08-28-138-193A-43

US-08-486-273A-43

US-08-480-474-43

US-08-440-095A-43

US-08-940-095A-43

US-08-940-095A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09130663A
Patent No. 6020163.
GENERAL INFORMATION:
TITLE OF INVERTION: LIPCCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130,663A
CURRENT FILING DAFE: 1998-08-05
FRIER APPLICATION NUMBER: 60/054,867
FRALIER APPLICATION NUMBER: 60/054,867
FRALIER FILING DAFE: 1997-08-06
SOFTWARE: FEALSE OF WINGOWS VERSION 3.0
SOFTWARE: FEASTED FOR WINGOWS VERSION 3.0
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99.8%;
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Best Local Similarity 99.8
Matches 515; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (7)...(516)
US-09-130-663-1
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US-09-130-663-1
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-467-693-1
US-08-467-693-1
US-09-130-663-16
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                                                                              AGGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 516
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Patent No. 6365716
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Best Local Similarity 99.88
Matches 515; Conservative
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ORGANISM: Homo sapiens
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NAME/KET: CDS

LOCATION: (7)...(516)

US-09-614-022-1
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US-09-614-022-1
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GENERAL INFORMATION:
APPLICARN: COMAIN, DAITELL C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER APPLICATION NUMBER: 09/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6143720
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (7)...(516)
US-09-432-335-1
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US-09-432-335-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.8%; Score 372.2; DB 3; Length 510; Best Local Similarity 59.6%; Pred. No. 1.7e-88; Matches 304; Conservative 117; Mismatches 89; Indels 0;
                                                                APPLICAMT: CORKIN, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130,663A
CURRENT FILING DATE: 1998-08-05
BARLIER PILLATON NUMBER: 66/054,867
RARLIER FILING DATE: 1997-08-06
SOFWARE: FASTERD FOR: 30
SOFWARE: FASTERD for Windows Version 3.0
SEQ ID NO 5
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; OTHER INFORMATION: n is any nucleotide
US-09-130-663-5
              Sequence 5, Application US/09130663A
Patent No. 6020163
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                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: variation
                                                      GENERAL INFORMATION:
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JS-09-130-663-5
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61 GARGARGARGAYATHACNGGNACNTGGTAYGTNAARGCNATGGTNGTNGAYAARGAYTY 120
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APPLICANT: CONAIIA, Darrell C.
TITLE OF INVENTOR: LIPCCALIN HOWOLOG
FILE REPERRACE: 97-24
CURRENT FILING DATE: 1997-11-02
COURRENT FILING DATE: 1997-11-02
RAMILER APPLICATION NUMBER: 09/13,613
FARLIER FILING DATE: 1998-08-06
FARLIER PILING DATE: 1997-08-06
SARLIER PLING DATE: 1997-08-06
SOFTHARE: FASTERQ POS: 30
SOFTHARE: FASTERQ FOR WINDOWS VERSION 3.0
FARMINE FOR SECTION OF STATES OF SECTION OF STATES O
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1. DOCATION: (1)...(510)
2. OTHER IRFORMATION: n is any nucleotide UC-09-432-335-5
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Patent No. 6365716

GRNEAL INFORMATION:
APPLICANT: CONklin, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
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ORGANISM: Artificial Sequence
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84 GCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 143
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FILING DATE: 1-Dec-99
FILING DATE: 13-Dec-99
FILING DATE: 13-Dec-99
FILING DATE: 13-Dec-99
FILING DATE: 14-Dec-96
FILING DATE: 16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DEC-16-DE
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COUNTRY: USA
ZIP: 02109
COMPUTER: USA
COMPUTER: ELADRAGIE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,603
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,549
BATTAN. DAMB.
                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
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                                                NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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Peptides from Dog
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                                                                                        CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 60/054,867
PRIOR APPLICATION NUMBER: 60/054,867
NUMBER OF SED ID NOS: 30
SOFTWARE: FastSED for Windows Version 3.0
SED ID NO 5
LENGTH: 510
CURRENT APPLICATION NUMBER: US/09/614,022 CURRENT FILING DATE: 2000-07-11
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APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins
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APPLICANT: Morgenstern, Jay P.
APPLICANT: Morgenstern, Jay P.
APPLICANT: Morgenstern, Jay P.
APPLICANT: Bill Andrew W.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog TITLE OF INVENTION: Dander and Uses Therefor NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 AACCAGGAGATTTTGGAACTCGCGCAGAGCGAAACCTGCTCCCAGGA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 GAGGAGGACATTICACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAA 551
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APPLICANTON NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORIEY/AGERT INFORMATION:
NAME: Wandragoures, Amy E.
REGISTRATION NUMBER: 36,207
REFERRENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
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APPLICATION MDEER: US/08/491,861A
FILING DATE: 27-0CT-1995
CLASSIFICATION: 435
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COMFUTER READMALE FORM:
MEDIUM TYPE: FLOPPY disk
COMFUTER: IRM FC compatible
SOFFWARE: ASCLI-Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08491861A
Patent No. 5939283
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TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 525 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
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       84 GCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 143
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                                                                                                 PADLICATION UNDER: US 08/156,549
FILING DATE: 22-NOY-1993
APPLICATION NUBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INTORNATION:
NUME: MANDER: 36,207
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: Allergenic Proteins and
1: Peptides from Dog
2: Dander and Uses Therefor
S: 104
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Braner, Andrew W.
TITLE OF INVENTION: Allergenic Proteins
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dender and Uses Then
NUMBER OF SEQUENCES: 104
CORRESPONDERS B. 104
ADDRESSEE: LAHIVE & COCKPIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII-text
CURREWA PAPLICATION DARA:
APPLICATION NUMBER: US/08/466,793
FILING DARE: 06-TUN-1995
CLASSIFICATION: 435
FROR APPLICATION: A35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
CAIP: 02109
CAIP: 02109
CAIP: 10209
COMPUTER: FIOPPY disk
COMPUTER: IN PC COMPALIBLE
COMPATER: FIOPPY disk
                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08466793 Patent No. 5891716
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1
FEATURE:
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US-08-466-793-1
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94.2%; Pred. No. 1.1e-11;
tive 0; Mismatches 5
                                                                                                                                                                                                                               Sequence 16, Application US/09432335
Patent No. 6143720
GERRAL HREOMATION:
TITLE OF INVENTION:
FILE REPERMER: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT PILING DATE: 1999-11-02
RABLIER PILING DATE: 1999-08-06
REALIER PILING DATE: 1997-08-06
REALIER PILING DATE: 1997-08-06
REALIER PILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE FILING DATE: 1997-08-06
SOFTWARE PILING DATE: 1997-08-06
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CURRENT APPLICATION WOMBER: US/09/614,022
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 60/054,867
PRIOR PLING DATE: 1997-08-06
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 147
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; OTHER INFORMATION: NEE-tagged linker
US-09-432-335-16
                                                         139 AGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                       122 AGGCCATGGTGGTCGATAAGGACTTT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: NEE-tagged linker US-09-614-022-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09614022 Patent No. 6365716 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 94.2
Matches 81; Conservative
                                                                                                                                                                                     RESULT 11
US-09-432-335-16
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US-09-614-022-16
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LENGTH: 147
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                                                                                                                                                                                                                Query Match 21.0%; Score 145.2; DB 2; Length 525; Best Local Similarity 60.0%; Pred. No. 4.3e.29; Matches 2B1; Conservative 0; Mismatches 178; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.3%; Score 78; DB 3; Length 147; Best Local Similarity 94.2%; Pred. No. 1.1e-11; Matches 81; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 GAGGAGGACAPTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAA 551
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CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 147
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APPLICANT: CORALIA,
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
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18-09-130-663-16
: Sequence 16, Application US/09130663A
: Patent No. 6020163
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ORGANISM: Artificial Sequence
                                                                                                         mat_peptide
79..525
                              CDS
1..525
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                      NAME/KEY:
; LOCATION:
US-08-491-861A-1
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67 GGTGGTCTTGTCCTTGACCCTGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 126
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tive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CORLIA, DETREIL C.
TITLE REFERENCE: 97-24
FILE REFERENCE: 97-24
GURRENY PELLICATION NUMBER: US/09/614,022
CURRENY FILING DATE: 2000-07-11
PRIOR PELLING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 09/130,63
PRIOR PELLING DATE: 1999-08-06
PRIOR PELLING DATE: 1999-08-06
PRIOR FILING DATE: 1997-08-06
SOFFWARE: FEASTERO for Windows Version 3.0
SEQ ID NO 24
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Job time : 55.2996 secs
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                                                                                                                                                                                                                           Sequence 24, Application US/09614022
Patent No. 6365716
                                                                                   127 AIGGIGGICGAIAAGGACITI 147
                                                            144 ATGGTGGTCGATAAGGACTTT 164
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Matches 78; Conservative
                                                                                                                                                                                                            US-09-614-022-24
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62 TGGAAGGTGTCTGTCCTTCACCCTGGAGGAGGAGATATCACAGGGACCTGGTACGTG 121
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Best Local Similarity 96.3%; Pred. No. 3.1e-11;
Matches 78; Conservative 0; Mismatches 3; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.0%; Score 76.2; DB 3; Length 147; Best Local Similarity 96.3%; Pred. No. 3.1e-11; Matches 78; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                            Sequence 24, Application US/09130663A
Fartent No. 6020163
GREERAL INFORMATION:
TITLE OF INTERTION:
FILE REPERBNCE: 97-24
GURRENT PAPLICANION ILLEPOCALIN HOMOLOG
FILE REPERBNCE: 97-24
GURRENT PAPLICATION NUMBER: US/09/130,663A
GURRENT FILING DAME: 1999-08-05
FARLIER PILING DAME: 1997-08-06
FARLIER PILING DAME: 1997-08-06
FARLIER PILING DAME: 1997-08-06
FORTHAMER OF SED ID NOS: 30
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TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
EARLIER FILING DATE: 1999-11-03
EARLIER FILING DATE: 1999-08-06
EARLIER FILING DATE: 1997-08-06
FARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRASE FOR IN NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: N-terminal Flag linker US-09-130-663-24
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                                                                                                          139 AGGCCATGGTGGTCGATAAGGACTTT 164
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                 RESULT 13
US-09-130-663-24
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84 GCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTAGAAGGCC 143

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Perfect score: Scoring table:

Title:

Run on:

Sequence:

Searched:

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sequence 59, App Sequence 2305, App Sequence 4, Appli Sequence 1855, App Sequence 1590, App Sequence 1590, App Sequence 1, Appli Sequence 43, Appli Sequence 43, Appli Sequence 43, Appli Sequence 53, Appli Sequence 54, Appli Sequenc
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APPLICANT: COLEN, MAURICE
APPLICANT: COLEN, MAURICE
APPLICANT: COLEN, MAURICE
APPLICANT: COLEN, TRACEN I.
APPLICANT: GORDON, JULIAN
APPLICANT: GORDON, JULIAN
APPLICANT: GORDON, JULIAN
APPLICANT: HODGES, STEVEN C.
APPLICANT: RANCCHYLL, JOHN C.
APPLICANT: REAGENTIC, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: THOMG
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST NUMBERS OF SEQUENCES: 27
CORRESPONDENCE: ADDRESS:
ADDRESSER: ADDRESS:
ADDRESSER: ADDRESS:
ADDRESSER: ADDRESS:
ADDRESSER: ADDRESS:
10 US-09-886-055-194

10 US-09-878-574-11281

10 US-09-878-574-59

10 US-09-878-574-59

10 US-09-878-574-305

10 US-09-878-574-305

10 US-09-878-574-306

10 US-09-878-574-306

10 US-09-959-82-4

10 US-09-959-82-4

10 US-09-917-800A-1590

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10 US-09-917-800A-1590

10 US-09-918-91-43

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COUNTRY: USA
ZIP: USA
ZIP: G0064-3500
COMPUTER READABLE FORM:
REDIOM TYPE: Diskette
COMPUTER: IBM COMPALIALE
COMPUTER: TRA COMPALIALE
SOFTWARE: FRSTERO, DOS
CURRENT APPLICATION NUMBER: US/09/099,823
FILING DATE: 20-UN-1997
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, CHEYJI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
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Patent No. US20020018990A1
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            Sequence 4, Appli
sequence 5, Appli
Sequence 803, Appli
Sequence 803, Appli
Sequence 1747, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 1, Appli
Sequence 17, Appli
Sequence 237, Appli
Sequence 25, Appli
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(without alignments)
6148.496 Million cell updates/sec
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692
1 GACGCCCAGTGACCTGCCGA......ATAAAGTCCTTCTCCCCCCA 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           816534
                                                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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10 US-09-983-381-1747

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10 US-09-099-823-3

10 US-09-099-823-1

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9 US-10-123-904-237

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9 US-10-123-904-237

10 US-09-884-847-1

10 US-09-884-847-17

10 US-09-884-887-17

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_NA:*
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Maximum Match 1100%
Listing first 45 summaries
                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Database:

Query Match 1

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Result

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                                                                                                                                                                                                             APPLICANT: STROUPE, STEPHEN D.
APPLICANT: YU, HOM
APPLICANT: YU, HOM
APPLICANT: YOU NEEDENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING STSTEM: DOS
SOFTWARE: FRASTEM: FOO SOFTWARE: FASTEN FOO WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
RILING DATE: US/09/099,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6120.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/879,354
TILING DATE: 20-UN-1997
ATTORNY ARREY INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
RERESENCE/DOCKET NUMBER: 5120.US.
TELECOMBUNICATION INFORMATION:
TELECOMBUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                COLPITTS, TRACET I.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                         KRATCCHTL, JON D. RUSSELL, JOHN C. SCHEFFEL, CHRISTI STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                       CUNTRY: IL
COUNTRY: USA
CIP: 60064-3500
CIP: GOORDIS READALE FORM:
MEDIUM TYPE: DISNette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGHTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott La
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-099-823-5
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                                                                                                                                                                                                                                                                                                                                                                                                        1 GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCC 60
                                                                                                                                                                                                                                                                                             Omery Match 100.0%; Score 692; DB 10; Length 692; Best Local Similarity 100.0%; Pref. No. 1.77-173 Matches 692; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120.US.Pl
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-099-823-5; Application US/09099823; Sequence 5, Application US/09099823; Patent No. US2002001899041; GENERAL INFORMATION: APPLICANT: BILLING-MEDEL, PATRICIA
                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-09-099-823-4
                                                                                                            TELEX:
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279 ATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTC 338

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APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090alel Nucleic Acid and Protein Homologs
TITLE OF INVENTION: No. US20020132090alel Nucleic Acid and Protein Homologs
CURRENT PAPLICATION NUMBER: US/09/833,381
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FeatsEQ for Windows Version 3.0
FRANCE ROBISON NOS: 2050
SOFTWARE: FeatsEQ for Windows Version 3.0
                                       339 ATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTTACTGCAAAGACCAGCAC 398
                                                       399 CATEGEGECCTECTCCACATGEGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTC 518
                                                                                                                                                                        249 ATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGGC 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 CACTACATCTTTACTGCAAAGACCAGCACCATGGGGGGCCTGCTCCACATGGGAAAGCTT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 GIGGGIAGGAATICIGAIACCAACCGGGAGGCCCIGGAAGAAITIAAGAAAIIGGIGCAG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 CGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 CGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 GIGICCCCAGIGAAGGIGACAGCCCTGGGCGGGGAAGIIGGAAGCCACGIICACCIIC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549 GAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.9%; Score 483.6; DB 10; Length 501; 99.0%; Pred. No. 1.5e-118; tive 0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                      482 ACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 517
                                                                                                                                                                                                                     519 ACCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 554
                                                                                                                                                                                                                                                                                                                          Sequence 803, Application US/09833381 Patent No. US20020132090A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.08
Matches 497; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-803
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US-09-833-381-803/c
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                                                                           421 GAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCCTGGAAGAATTTAAGAAAT 480
                                                                                                                                    601 ACACAGAGCCCGGACCACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCC 660
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTGGTCGATAAG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 CTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AGCCIGGCAAATACAGCGCCTAIGGGGGCAAGCTCAIGTACCIGCAGGAGCIGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.3%; Score 514.4; DB 10; Length 523; 99.8%; Pred. No. 1.1e-126; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lok, Si
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
TILLE OF INVENTION: Use of Human Phermone Polypeptides
FILE REFERENCE: 00-85
CURRENT APPLICATION NUMBER: US/09/951,845
CURRENT APPLICATION NUMBER: 2001-09-12
NUMBER OF SEQ. ID NOS: 5.
                                                                                                                                                                                                                                                                                                                                                           ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
                                                                                                                                                                                                                                                                                                                                                                            661 ACCTGACTCCAAATAAAGTCCTTCTCCCCCCA 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09951845 Patent No. US20020098497A1 GENERAL INFORMATION:
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Best Local Similarity 99.8'
Matches 515; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (8)...(517)
US-09-951-845-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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Sequence 1747, Application US/09833381
Sequence 1747, Application US/0983381
Farent No. 192202013090A1
GENERAL IMPORMATION:
THIS OF INVENTION:
THIS OF INVENTION:
THIS OF INVENTION:
THIS OF INVENTION NUMBERS 5800-119
FILE REFERENCE: 5800-119
FILE REFERENCE: 2800-119
FILE REFERENCE: 2001-04-11
FRIOR FILING DATE: 2001-04-11
FRIOR PILING DATE: 2000-02-99
NUMBER OF SEQ ID NOS: 2050
SOFTHARE: FRASEEN FOR WINDOWS VERSION 3.0
SEQ ID NO 1447
LERNGTH: 336
                                                                                                                       414 CACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACGGGGGGCCCTGGAAGAATTT 473
                                    534 GGAAGCTGCGTTCCCGAACACTAGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCTA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGGGGAAGTTGGAAGCCACGT 240
                                                                                                                                                                                                                                                                                                                                                                                594 CCACCAGACACAGAGCCCGGACCACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCT 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AGGGACCTGGTA-CGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 ccassaaserereceasrsaassrsaasereaceressessaasrrssaaseraser 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TCACCTTCATGAGGAGGATCGGTGCATCCAGAAGAAATCCTGATG-CGGAAGACGGAG 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          654 CCCACCCACCTGACTCCAAATAAAGTCCTTCTCCCCC 690
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US-09-099-823-2
; Sequence 2, Application US/09099823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-833-381-1747
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US-09-833-381-1747
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354 CTGCCCAGGAGGGACCACTACATCTTTTACTGCAAGACCAGCACCATGGGGGCCTGCTC 413
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APPLICANT: KRATCCHVIL, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEPLE, JOHN C.
APPLICANT: STEPLEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL.
TITLE OF INVENTION: POR DEFECTING DISEASES OF THE BREAST NUMBER OF SEQUENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCES: ADDOLT 1. P. P. C. C. STEPLEN D.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 337
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48.7%; Score 337; DB 10; Length 3:
Best Local Similarity 100.0%; Pred. No. 6.2e-80;
Matches 377; Conservative 0; Mismatches 0; Indels
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COMPUTER: IN Compatible
SOFTWARE: FastExE for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/099,823
FILING DATE:
CLASSIFICATION NAMBER: 08/09/099,823
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6120.US.P1
                                                                                                                                                                                                                                                                                                               S-09-099-823-3/c
Sequence 3. Application US/09099823
Patent No. US20020018990A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COHEN, MAURICE
APPLICANT: COHEN, MAURICE
APPLICANT: COHENTS, TRACET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                          669 CCAAATAAAGTCCTTCTCCCCC 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLPITIS, TRACEY L. FRIEDMAN, PAULA N.
                                                                                                                                                              CCAAATAAAGTCCTTCTCCCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRRACTERISTICS:
LENGTH: 337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Abbott Park
STATE: IL
COUNTR: USA
ZIP: 60064-3500
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-09-099-823-3
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APPLICANT:
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61 TGGGTGTCACGCTCGGCCTGGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACGCCCAGTGACCTGCCGAGGTCGGCAGCAGCAGAGCTCTGGAGATGAAGACCCTGTTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KRATOCHVIL, JON D.
APPLICANT: RUSSELL, JUHN C.
APPLICANT: SCHENFEL, OHRISTI
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: TV, HONG
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.1%; Score 236; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.5e-53;
Matches 236; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPREATIG SYSTEM: DOS
SOFTWARE: FrastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLNG DATE: US/09/099,823
FILLNG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6120.US.P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 35,441
FERERENCE/DOCKET NUMBER: 35,441
FERENCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSES: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                         RESULT 8
12-09-099-823-1
15-09-009-823-1
2 Sequence 1, Application US/0909823
Patent No. US2002001899001
                                                                                                                                                                                                                                                            COLPITYS, TRACET L. FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                     VANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                              HODGES, STEVEN C
KLASS, MICHAEL R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 236 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                     JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3S: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 60064-3500
                            241 GCTGC 245
353 GCTGC 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 GACGGAGGAGCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                      APPLICANT: KRATOCHVIL, JON D.

APPLICANT: RUSSELL, JOHN C.

APPLICANT: SCHEFFEL, CHRISTI

APPLICANT: STROUPE, STEPHEN D.

APPLICANT: XU, HONG

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST

NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FORSESE OF Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Becker, Cheryl L.
REGISTRATION UNBER: 35,441
REFERENCE/DOCKET WOMER: 6120.US.Pl
FELECOMUNICATION INPORMATION:
TELEPHONE: 847/935-1729
                                         BILLING-MEDEL, PATRICIA COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UNN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                COLPITYS, TRACET L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 base pairs
Patent No. US20020018990A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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STATE: ID
COUNTRY: USA
-7. 60064-3500
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US-09-099-823-2
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us-09-099-823-5.rnpb

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GENERAL INFORMATION:

APPLICANT: HO, SONG CT AL

APPLICANT: HO, SONG CT AL

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

TITLE OF INVENTION: USES THERROF

FILE: REFERENCE: CL001237

CURRENT APPLICATION NUMBER: US/10/143,576

CURRENT FPLIKG DATE: 202-05-13

NUMBER OF SEQ ID NOS: 6

SOTTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO.1
                          264 TGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTAT 323
                                                                                                                                                                             324 GGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTAC 383
                                                                                                                          232 TGCCAGRACATCACGGTGGTCCTGCAAAAACCTCTGAGCCTGGCAAATACACGGCATAC 291
                                                                                                                                                                                                     384 IGCAAAGACCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCT 443
                                                                                                                                                                                                                                                                                 444 GATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AAIGCIGAAAAGTICICAGGCCICIGGTACGIGGCICCCAIGGCAICTGCACGGGGC 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 TTTCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 Trocresecadadeaccacorerererecadeaceaeceaeceaeceaeceaeae 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 GGGGCCTCCACATGAATTCCCGGGGGCGGACGCTGTAACCAGGTGGATGCC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CIGAIGCGGAAGACGGAGGAGCCIGGCAAAIACAGCGCCIAIG---GGGGCAGGAAGCIC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 GAGTACCTGAAGGTGGGCTCCGAGGBACACTTCAGAGTCCCGGCCTTGGGCTACCTGGAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AIGTACCIGCAGGAGCIGCCCAGGAGGGACCACIACAICTITIACIGCAAAGACCAGCAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%; Score 54.8; DB 9; Length 555;
46.6%; Pred. No. 2.1e-05;
tive 0; Mismatches 277; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      504 GAGGAGGACATITICACGCCCTGCAGACGGGAAGCTGCGTTCCCGAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10143576
Publication No. US20030013151A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.9%
Best Local Similarity 46.6%
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-143-576-1
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US-10-143-576-1
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84 GCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ATGGTGGTCGATAAGGACTTTCCGGAGGACGAGGCCCAGGAAGGTGTCCCCAGTGAAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCTGGGCGGTGGGAAGTTGGAAGCC 236
                                                                                               APPLICANT: Morgenstern, Jay D.
APPLICANT: Morgenstern, Jay D.
APPLICANT: Railecary, Andreay
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
NUMBER OF SEQUENCES: 104
CORRESPONDENCES: 104
ADDRESSEB: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 21.0%; Score 145.2; DB 10; Length Best Local Similarity 60.0%; Pred. No. 2.9e-29; Matches 281; Conservative 0; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Auy R.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELECOMMOULACHION INCREMITON:
TELEFENE (617) 227-7400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THA PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,861
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                              Sequence 1, Application US/09374671
Patent No. US20020012963A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 525 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide 79..525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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NAME/KEY: CDS
LOCATION: 1..52
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
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US-09-374-671-1
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US-09-374-671-1
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APPLICANT: Hathur, Barlan
APPLICANT: Hathur, Barlan
APPLICANT: Hathur, Carlan
APPLICANT: Hathur, Carlan
TITLE OF INTENTION: No. US20020107375A1e1 Human Lipocalin Homologs and Polynucleo'
TITLE REFERENCE: LEX-0173-USA
CURRENT PAPLICATION NUMBER: US/09/854,847
CURRENT PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 60/203,874
PRIOR APPLICATION NUMBER: US 60/203,874
NUMBER OF SED ID NOS: 20
SOFTWARE: PASIENCY for Windows Version 4.0
SED ID NO 9
ENGURENT FIRST CARLAND NOS: 20
ENGURENT FOR STORE OF THE NUMBER OF SED US NOS: 20
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APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020107375Alel Human Lipocalin Homologs and Polynucleot
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46.6%; Pred. No. 2.1e-05;
Live 0; Mismatches 277; Indels 6
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                                                                                                                                                                                                              ;) Sequence 9, Application US/09854847
;) Patent No. US20020107375A1
;) GENERAL INFORMATION:
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; ORGANISM: homo sapiens
US-09-854-847-9
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US-09-854-847-9
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Sequence 1, Application US/09854847
Batent No. USS/0020107375A1
GENERAL INFORMATION:
APPLICANT: Mathur, Brian
APPLICANT: Mathur, C. Alexander Jr.
TITLE OF INVENTION: NO. US20020107375A1e1 Human Lipocalin Homologs and Polynucleotide
FILE REFERENCE: LEX-0173-USA
CURRENT APPLICATION NOMBER: US/09/854, 847
CURRENT APPLICATION UNGER: 2001-09-10
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 28
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                                                399 CATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAG 458
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US-09-854-847-1
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CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
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R APPLICATION NUMBER: 60/059122
JR FILING DATE: 1997-09-17
R APPLICATION NUMBER: 60/059184
OR APPLICATION NUMBER: 60/059184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION UNDER: 66/062814
PRIOR PELICATION NUMBER: 60/062814
PRIOR PELICATION NUMBER: 60/06316
PRIOR PELICATION NUMBER: 60/063145
PRIOR PLICATION NUMBER: 60/063145
PRIOR PLICATION NUMBER: 60/063182
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-31
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R APPLICATION NUMBER: 60/063738

R APPLICATION NUMBER: 60/063738

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/064248

R APPLICATION NUMBER: 60/064248

R APPLICATION NUMBER: 60/064289

R APPLICATION NUMBER: 60/064809

R APPLICATION NUMBER: 60/064809

R PELING DATE: 1997-11-07

R PELING DATE: 1997-11-07

R PELING DATE: 1997-11-07
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RA APPLICATION NUMBER: 66/063329
RA PLILING DATE: 1997-10-27
RA APPLICATION NUMBER: 60/063550
RR FILING DATE: 1997-10-28
RA APPLICATION NUMBER: 60/063561
RR FILING DATE: 1997-10-28
                                                                                                                                          CURRENT FILING DATE: 2001-12-19
ERICR APPLICATION NUBBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
                                                                                                                                                                                                                         APPLICATION NUMBER: 60/059113
TOTAL DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059117
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FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/062285
FILING DATE: 1997-10-17
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FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/065846
FILING DATE: 1997-11-17
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FILING DATE: 1997-11-21
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       Watanabe, Colin
Wood, William
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FILING DATE: 1997-09
                                                    APPLICANT: Zhang
FITLE OF INVENTION:
FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                         45 ATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGCCCGCTGCCCTTTCACCCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AICCIGACCIGCICIGGCCCCACGCTCAGGCTGAGGITCTGCTGCAGCCTGACTIC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGG---TGGTCGATAAGGAC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 GGGAAGTTGGAAGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATG---GGGGCAGGAAGCTC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 ATGTACCTGCAGGAGCTGCCCAGGAGGACCACTACATCTTTACTGCAAAGACCAGCAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 GIGCGCATCGIGGACACAGACTACAGCICCITCGCCGICCTITACATCIACAAGGAGCIG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 CATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGGTAGGAATTCTGATACCAACCGGGAG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 GAGGGGGCGCTCAGCACCATGGTGCAGCTCTACAGCCGGACCCAGGATGTGAGTCCCCAG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTC 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 GCTCTGAAGGCCTTCCAGGACTTCTACCCGAGGCTCCCCCGAGGACATGATGGTC 546
                                                                                                                                                                                                                                                                                                Query Match 7.9%; Score 54.8; DB 10; Length 597;
Best Local Similarity 46.6%; Pred. No. 2.1e-05;
Matches 247; Conservative 0; Mismatches 277; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 TTTCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519 ACCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547 ATGCTGCCCCAGTCAGATGCAACCCTGAGAGCAAGGAGCGCCCTG 596
PILE REPERENCE: LEX-01/3-USA
CURRENT APPLICATION NUMBER: US/09/854,847
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 60/203,874
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FESLSEQ for Windows Version 4.0
ESC ID NO 17
LENGTH: 597
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Publication No. US20030004311A1
GENERAL INFORMATION:
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Gerritsen, Mary E.
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Stewart, Timothy F
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beresini, Maureen
DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: homo sapiens
US-09-854-847-17
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US-10-028-072-237
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PRIOR FILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR PRICATION NUMBER: 60/084600
PRIOR PILING DATE: 1998-05-07
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RETLING DATE: 1998-02-09

RAPPLICATION NUMBER: 60/07791

RAPPLICATION NUMBER: 60/078910

RAPPLICATION NUMBER: 60/078910

RETLING DATE: 1998-03-20

RETLING DATE: 1998-03-25

RETLING DATE: 1998-03-27

RETLING DATE: 1998-03-25

RETRING DATE: 1998-0
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RAPICATION NUMBER: 60/08129

RETLING DATE: 1998-04-09

RAPICATION NUMBER: 60/081695

RAPICATION NUMBER: 60/081695

RAPICATION NUMBER: 60/081817

RETLING DATE: 1998-04-15

RAPICATION NUMBER: 60/081918

RETLING DATE: 1998-04-15

RAPICATION NUMBER: 60/081918

RETLING DATE: 1998-04-24

RAPICATION NUMBER: 60/081918

RETLING DATE: 1998-04-24

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PRIOR PLILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
                                                                                                                                                                                         PRIOR FILING DATE: 1997-11-24
PRIOR PELICAPION NUMBER: 66/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/069278
PRIOR PLITME DARE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/06934
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1397-12-16
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PRIOR FILING DATE: 1998-01-23
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RIOR APPLICATION NUMBER: 60/081203
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ING DATE: 1998-05-13
LICATION NUMBER: 60/085339
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066511
FILING DATE: 1997-11-24
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NG DATE: 1997-12-16
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APPLICATION NUMBER: 60/085323
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/08106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
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PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07

Query Match 7.7%; Score 53.2; DB 9; Length 762; Best Local Similarity 46.4%; Pred. No. 6.1e-05; Matches 246; Conservative 0; Mismatches 278; Indels 6; Gap

230 GGCGCCTCCACGTCCACATGCAGTTCCCCGGGCGGGCGGCTGTAACCAGGTGGATGCC 289 410 GAGGGGCCCTCACCATGGTGCAGCTCTACAGGACCCAGGATGTGAGTCCCCAG 469 162 TITCCGGAGGACGACGCCCAGGAAGGTGTCCCCAGTGAAGGTGACGTCACCCTGGGCGGT 221 282 CTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATG---GGGGCAGGAAGCTC 338 290 GAGTACCTGAAGGTGGGCTCCGAGGGACACTTCAGAGTCCCGGCCTTGGGCTACCTGGAC 349 339 ATGTACCTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTACTGCAAAGACCAGCAC 398 399 CATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAG 458 45 ATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTG 104 105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGG---TGGTCGATAAGGAC 161 222 GGGAAGTTGGAAGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAATC φ 셤 윱 δ 셤 δŽ δ 셤 20

459 GCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTC 518

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519 ACGCCCCTGCAGACGGGAAGCTGCCCGAACACTAGGCAGCCCCCGG 568
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ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33301C17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 GAGGAGGAGGATATCACAGGGACCTGGTACGTGAAGGCCATGG---TGGTCGATAAGGAC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 TITCCGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 GGGAAGTIGGAAGCCACGTICACCTICAIGAGGAGGAICGGIGCAICCAGAAGAAATC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 CTGATGCGGAAGACGGAGCCTGGCAAATACAGCGCCTATG---GGGGCAGGAAGCTC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 GAGTACCTGAAGGTGGGCTCCGAGGGACTTCAGAGTCCCGGCCTTGGGCTACCTGGAC 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 AIGIACCIGCAGGAGCIGCCCAGGAGGACCACTACAICTITTACTGCAAAGACCAGCAC 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.7%; Score 53.2; DB 9; Length 762; Best Local Similarity 46.4%; Pred. No. 6.1e-05; Matches 246; Conservative 0; Mismatches 278; Indels
                                            519 ACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGG 568
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CURRENT PILING DATE: 2002-04-12
CURRENT PILING DATE: 2002-04-12
CURRENT OF SEQ ID NOS: 550
LD NO 237
LENGTH: 762
                                                                                                                                                       Sequence 237, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe, Colin R
                                                                                                                                                                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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; ORGANISM: Homo Sapien
US-10-121-049-237
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337 48.7 337 9 AA460323 AA460323 AA460323 239.2 47.6 349 9 ALI43970 ALI222 ALI877465 ALI877465 ALI877465 ALI877465 ALI877465 ALIA77465 ALIA7774 ALIA774 ALIA77	BE596144 BE759514 BE759514 BE761244 BE76124 BE76123 Y BE76529 BE7657509	RESULT 1 AW513637/C LOCUS AW513637/C LOCUS AW513637 AUGAP_ULI Homo sapiens cDNA clone IMAGE:27071713' Similar to TR:063613 Q63613 ODORANT-BINDING PROTEIN: ; mRNA ACCESSION WESIGN WEST WEST WESIGN WEST WES
o o o o o o o o o o o o o o o o o o o		d, 100.x 100.x 100.x 111.s
n 5.1.3 Compugen Ltd. Search time 1923:58 Seconds (without alignments) 5826.269 Million cell updates/sec	32308132	cted by chance to have a score distribution. Description AM513637 X047h10.X AM51363
Gencore versic (c) 1993 - 2003 using sw model 2003, 22:05:36 3-5 GACCIGCCGA Gapext 1.0	of hits satisfying chosen parameters: q length: 2000000000 q length: 2000000000 ng: Minimum Match 100% Maximum Match 100% Lighting first 45 summaries EST: 4 summaries EST: 4 summaries : em_esthm:* 3: em_esthm:* 5: em_esthu:* 6: em_estru:* 7: em_estru:* 9: ep_estr:* 10: qp_estr:* 11: qp_hte:*	sults predict the total structure to the total structure summaries summaries 451747 47508 460385
Copyright (OM nucleic - nucleic search, Run on: February 9, Title: US-09-099-823 Sequence: 692 Sequence: 1 GACGCCCAGTC Scoring table: IDENTIT_NUC Gapop 10.0 , Searched: 16154066 segs	Total number of hits satisfying chosen paraminimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries Egr: Maximum Match 100% Listing first 45 summaries Egr: Acceptant: 1: em_estha: * 2: em_estha: * 3: em_estha: * 4: em_estru: * 5: em_estru: * 6: em_estru: * 7: em_estru: * 8: em_htc: * 10: qb_est: * 10: qb_est: * 11: qb_best: * 11: qb_best: * 11: qb_best: *	12. gb_est3:* 13. gb_est4:* 14. gb_est4:* 14. gb_est4:* 15. em_estfun:* 15. em_estfun:* 17. gb_gss_lnn:* 17. gb_gss_lnn:* 18. em_gss_lnn:* 20. em_gss_lnn:* 21. em_gss_lnn:* 22. em_gss_lnn:* 24. em_gss_lnn:* 25. em_gss_lnn:* 26. em_gss_lnn:* 27. em_gss_lnn:* 27. em_gss_lnn:* 28. em_gss_lnn:* 28. em_gss_lnn:* 29. em_gss_lnn:* 20. em_gss_ln:* 20. em_gss_ln:

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E 1 (bases 1 to 513)

S NII-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Carcer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

U Dopublished (1997)
Contact: Nobert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@lamge.lln].00
Insert Leongortium (info@lamge.lln].00
Seq primer: -40ml3 fwd. Error: 0.00
Seq primer: -40ml3 fwd. Err from Amersham
High quality sequence stop: 339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 ACTGAGGGAGGATAGGTGCATCCAGAAGAAAATCCTGATGCGGAAGAGGGGAGGGCTGG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 TGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 A-TGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 CAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 CCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGGCCTGCTCCACATGGGAAAGCT 427
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: uterus; Vector: pcMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 145 c 159 g 139 t 2 others
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Bomo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586 CCACCCTACCACACACACACAGGGCCCGGACCTGGACCTACCCTCCAGCCATGACCCT 645 `
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.1%; Score 499; DB 10; Length 532;
96.8%; Pred. No. 2.6e-110;
Live 0; Mismatches 17; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 CGGAGGACAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGA 225
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AA977608
AA977608.1 GI:3155054
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1. .532
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Matches 508; Conservative
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 36 Std Error: 0.00
Seq primer: 40UP from Glbco
High quality sequence stop: 330.
Location/Qualifiers
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/ Lab_bost="Thats=#4xxxx:9606"
/ Lab_bost="Thats=#4xxxxx:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 499)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP intp://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
586 CCACCCTACCACACACACAGAGCCCGGACCAGGACCTACCCTCCAGCCATGACCT 645
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                                                                                                                                                                                                                                                                                                                                                    499 bp mRNA linear EST 30-NC q024d02.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845603 3' similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN: , MRNA sequence. A1219510.1 GI:3801713
                                                                                                                   Query Match 65.4%; Score 452.8; DB 9; Length 499; Best Local Similarity 94.2%; Pred. No. 3.8e-99; Matches 469; Conservative 0; Mismatches 29; Indels 0;
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135 c 151 g 126 t
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                                                                                                                          EST 05-NOV-1998
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Babai: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
High quality sequence stop: 396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 AGTTGGAAGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 GCCTGCTCCACATGGGAAAGCTTGTGGGGTAGGAATTCTGATACCAACGGGAGGCCCTGG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                   dp90F12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854287 3 similar to TR:063613 Q63613 ODORANT-BINDING AT251747, mRNA sequence.
A1251747.1 GI:3848276
BSP.
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/organism="Nemo sapiens"
/db_xref="texon:9606"
/clone="liAngs:1844287"
/clone=lib="Soarse=NEL_T_GBC_S1"
/lab_host="PH108"
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Elkaryota, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
El (bases 1 to 4) Marional Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Contact: Robert Strausberg, Ph.D.
Empiblished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs:r@mil.nih.gov
This clone is available royalty-free through LINE; contact the IMAGE Consortium (info@image.llni.gov) for further information.
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 344.
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(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                277 AAATCCTGATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGGCAGGAAGC 336
                                                                                                                                                                                                                                                                                                                        337 TCATGTACCTGCAGGAGCTGCCCAGGAGGACCACTACATCTTTACTGCAAAGACCAGC 396
                                                                                                                                                                                                                                                                                                                                                                                                      397 ACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGG 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 ICACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCAC 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AAAACCTGAIGCGGAAGAGGGGGGGGGCTGGCAAAIACAGGGCGCTAIGGGGGGAAGAAGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · 304 CICCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCTGGACCTACCCCCCCAGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A31 bp mRNA linear EST 29-Al on'5fil.s1 Soares NFL T GBC, S1 Homo sapiens CDNA clone IMAGE:1562541 3' similar to TR:Q63613 Q63613 ODORANT-BINDING PROFIEN. ', mRNA sequence.
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/clone_lib="soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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1 (bases 1 to 415)

11 (bases 1 to 415)

12 (bases 1 to 415)

13 (bases 1 to 415)

14 (bases 1 to 415)

15 (bases 1 to 415)

17 (and bar, L., Alben, M., Leanon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wille Washu-Merck Esf Project 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Far: 314 286 1810
Far: 34 286 1810
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is
Seq primer: -28m13 rev2 EF from Amersham.
Location/Qualifiers
                                              434
                                                                 119 GICTITIACIGEAAAGACCAGCGCCGTGGGGCCTGCGCTACATGGGAAACCTGTGGGGT 260
                                                                                                                            435 AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAG 494
                                                                                                                                                    555 TAGGCAGCCCCGGGTCTGCACCTCCAGAGCCCACCTACCACAGACACAGAGCCCGGA 614
  495 GGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC 554
                                                                                                                                                                                                                                                                                                                                                                                  615 CCACCTGGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCCACCTGACTCCAAAT 674
                                                                                                                                                                                                                                                                                                                          79 CCACCTAGGACCTACCAGCCATGACCCTTCCCTGCTCCCACCTGACTCCAAAT 20
                                           375 ATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
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/db_xref="GDB:6039283"
/db_xref="taxon:9606"
/clone="IMAGE:795778"
/clone_lib="Soares_testis_NHT"
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AA460385.1 GI:2185598
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Kammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 349)
Tel: 314 286 1800

Fax: 314 286 1810

Fax: 314 286 1810

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seg primer: -4nml3 fwd. RT from Amersham High quality sequence stop: 323.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 Crecccadeadecaccactacarcritracrecaaagaccagcaccareegegecorecre 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414, CACATGGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 AAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 GGAAGCTGCGTTCCCGAACACTAGGCAGCCCCCGGGTCTGCACCTCCAGAGCCCACCTA 593
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                                                                                                                                                                                                                                                                                   1.337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db xref="taxon:9606"
/clone="Imags:795778"
/clone="Imags:Lestis_NHT"
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AI143970.1 GI:3665779
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Bukaryota Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 337)

15 Hillier, L., Allen,M., Bowles, L., Dubuque,T., Geisel,G., Jost,S.,

Kucaba,T., Lacy,M., Lennon,G., Marra,M., Martin,J., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie

"T. Materston,R. and Wilson,R.

Mashir-Merok EST Project 1997

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBL139W, restis NRT, and B-cell NVI_CGAP_CGNI) were mixed, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687339, T26468-728711, and 729056-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA460323 337 bp mRNA linear EST 09-JUN-1997 2X51060; and close Lestis_NHT Hono sepices continued continue 199778 3' similar to TR:@207551 ©100RANT-BINDING PROTEIN. ', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 TCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCA 560 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 TATGGGGCAGGAAGCTCAIGTACCIGCAGGAGCTGCCCAGGAGGGACCACTACATCTTT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 TACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGTAGGAAT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 GCCCCCGGGTCTGCACCTCCAGAGCCCACCTACCACCAGACACAGAGCCCGGACCACCT 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 TACTGCAAAGACCAGCGCCGT-GGGGCCTGCGTACATGGGAAAGCTTGTGGGTAGGAAT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 TCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGACTC 500
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AA460323.1 GI:2185139
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Gaps

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Length 337;

86

us-09-099-823-5.rst

AUTHORS TITLE JOURNAL

FEATURES

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ESM Mus musculus
Enkaryota, Metazoa; Choxdata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 603)
Rarkawa, T., Carninoi, P., Fukuda, S., Puruno, M., Hanagaki, T., Hara, A.,
R., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kondo, H., Kouda
(M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Roya, S., Matsuyama, T., Miyazaki, A., Sano, H., Sasaki
(D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Sano, H.,
Ragama, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y., et al. 2001)
All Dupublished (2001)
Contact: Voshihide Hayashizaki, Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
W. Konno,H. Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wafi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
N.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashiaaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Bunan Genome Sequences. Marm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, 6 days neonate head"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="head"
/dev_stage="6 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/63"
/db_xref="taxon:10090"
/clone="5430417003"
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(Pharmacia), digested with Not I and cloned into the Not I
and Bco RI sites of the modified pr773 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
80 c 115 g 99 t
                                                                                     Tumor Gene Index
published (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nh.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
                                                                                                                                                                                                                                                                                                                 CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-GGP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMT at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
1. .349
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             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 CAGGAGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACAT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 GGGAAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAA 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1737716"
/clone_lib="Soares_testis_NHT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant CNM library. Genome Res. 11 (2), 281-289 (2001) Rondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                             On Jun 8, 2000 this sequence version replaced g1:8383516.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9226
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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/strain="657BL/64"
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/nlone="543047703"
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3/]. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end:
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 626)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 ACGCTCGGCCTGGCCGCTGCCTTCACCCTGGAGGAGGATATCACAGGGACC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 AAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGAC 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 CINGIGGGIAGGAANTCTGATACCAACCGGGAGGCCCIGGAAGAATTTAAGAAATTGGTG 485
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                                                                                                                                                                                                                                                                                                                                                                                                    9 GTGACCTGCCGAGGTCGGCAGCACACAGAGCTCTGGAGATGAAGACCCTGTTCCTGGGTGTC 68
                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                          24.7%; Score 171.2; DB 10; Length 603; 58.3%; Pred. No. 4.6e-31; ive 0; Mismatches 238; Indels 4;
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BB028765.2 GI:16258092
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                                                                                                                                                                                                                                                                                       Best Local Similarity 58.3
Matches 338; Conservative
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/note="Organ: uterus; Vector: pT773D-Pac (Pharmacia) with a modified PoJ1inker; 1st strand cDNs was prepared from pregnant mouse uterus, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNs was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonalo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R47029 15-MAY-1995 15-MAY-1995 15-MAY-1995 15-MAY-1995 15-MAY-1995 Nat incisor (noncalcified tissues) Rattus norvegicus CDNA clone 1358 5' end similar to odorant-binding protein (RYZG12), mRNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;

    (bases 1 to 494)
    Matsuki, Y., Nakashima, M., Amizuka, N., Warshawsky, H., Goltzman, D., Yamada, K. M. and Yamada, Y.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 GGTGGGAAGTTGGAAGCCACGTTCACCTTCATGAGGAGGATCGGTGCATCCAGAAGAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 TTCGTGATGAAGAAAACAGAAGACCTGGCAAATACACCGCTTTTCATAACACGAAGGTT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 ATTCATGTGGAAAAGACGTCGGTGAATGAGCACTACATTTTCTACTGCGAAGGCCGGCAC 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 CTGGAGATGAAGACCCTGTTCCTGGGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTC 98
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                                                                                                                                                                                                                                                                                                                                                      23.4%; Score 162.2; DB 9; Length 519; 59.6%; Pred. No. 6.7e-29; ive 0; Mismatches 194; Indels 3
/clone_lib="Soares_NMPu"
/sex="female"
                                             /dev_stage="adult"
/lab_host="DH10B"
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Matches 291; Conservative
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R47029
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                                                  ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 51)
NOI-CRAP http://www.nobi.nlm.nih.gov/noicgap.
NOI-CRAP http://www.nobi.nlm.nih.gov/noicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nib.gov
This clone is available royalty-free through LiNL; contact the
LINGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                   126 GACTIGGAGACCACAGIIGTAITCIGGAACAAIGGICATIGCCGIGAGIITAAAITCGIG 185
                                                Gaps
                                                                                           105 GAGGAGGAGATATCACAGGGACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTT 164
                                                                                                                                                                                        165 CCGGAGGACAGGAGGCCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGG 224
                                                                                                                                                                                                                                                                                 225 AAGTIGGAAGCCACGTICACCITCAIGAGGAGGAICGGIGCAICCAGAAGAAATCCIG 284
                                                                                                                                                                                                                                                                                                                                                                         285 ATGCGGAAGACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCCAGGAAGCTCATGTAC 344
                                                                                                                                                                                                                                                                                                                                                                                                      404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 GCCTG---CICCACAIGGGAAAGCITGTGGGGTAGGAATICTGATACCAACCGGGAGGCC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 ACGTCGTCATTCGGGATGGGAAAAGCTCATGGGGAAAACTCTGGTGAAAATCCAGAGGCC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 CIGGAAGAAITITAAGAAATIGGIGCAGCGCAAGGGACTCICGGAGGAGGACAITITICACG 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 CCAGAGATCGGAGATAAATGTGTTGAAAGTGACTAGGCAGCTACCCAGGTCTGCAACAGC 485
                                                                                                                        6 GACCIGGIGGATTACICIGGGACTGGTACGCAAAGGCCATGGTACACAATGGTACCCTA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522 CCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGGCAGC-CCCCGGGTCTGCACCTCC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 CTGCAGGAGCTGCCCAGGAGGGACCACTACATCTTTTACTGCAAAGACCAGCACCATGGG
                                                  4;
     DB 10; Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581 AGAGCCCACCTACCACCAGACACAGAGCCCGGACCACCTGGACCTACCCTC 632
Score 169.6; DB 10; Length
Pred. No. 1.1e-30;
0; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative full length read
vector to vector length is
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 503.
Location/Qualifiers
1..519
/Organism="%mass musculus"
/Dxef="laxon:10090"
/Clone="Image:1434777"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI877465
AI877465.1 GI:5551514
  24.5%;
60.0%;
                     Best Local Similarity 60.09
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Onpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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  Query Match
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
Single pass sequencing. Bases called and alt_trimmed with the -minscore 18
and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                             1 (bases 1 to 337)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovines; Bos.
                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adranl, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 CTGCCCT------GTCCTTCACCCTGGAGGAGGAGGATATCACAGGGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 cceccreaegecccaggagcccccgrccrgcccrgrggagccccagcagarcgcagga 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 CCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGACGCCCAGGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 AGGIGICCCCAGIGAAGGIGACAGCCCIGGGCGGIGGGAAGIIGGAAGCCACGIICACCI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 148; DB 12; Length 337;
Pred. No. 1.6e-25;
0; Mismatches 85; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                     USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
/clone_lib="MARC_2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 GCAAATACAGCGCCTATGGGGGCAGGAAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 GCGAATACAGCTCCAATGGCGGCAAGAAGC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 76 row: C column: 21
Seq primer: ATTTAGGTGACATATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
                      GI:11077252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.4%;
Best Local Similarity 68.8%;
Matches 227; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
                      BF193883.1
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     BF193883
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                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib=nat incisor (noncalcified tissues)*
/clone_lib=nat incisor (noncalcified tissues)*
/lab_host="Xr.1 blue"
/note="vector: Bluescript II SK -; Site_1: Eco RI; Site_2:
/note="vector: Bluescript II SK -; Site_1: Eco RI; Site_2:
Xho I; The apical portion and the entire pulp of the
maxillary and mandibular incisors from 3-4 week old rats
were excised. A cDNA library was constructed in the liap
II vector (Stratagene) by use of poly A+ RNA from these
tissues. The phage cDNA library was converted into a
Bluescript phagemid cDNA library by in vivo excision by
the Exassist/Solm system (Stratagene).

45 a 101 c 144 g 96 t
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compilation of partial sequences of randomly selected cDNA clones
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                                                                                                             Laboratory of Developmental Biology, National Institute of Dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 CCTGTTCCTGGGTGTCACGCTCGGCCTGCCTGCCCTGTCCTTCACCCTGGAGGAGI12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GGATATCACAGGGACCTGGTACGTGGAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 CAGGAGGCCCAGGAAGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AGCCACGTTCACCTTCATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 GACGGAGGAGCCTGGCAAATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 GCTGCCCAGGAGGGACCACTACATCTTTACTGCAAAGACCAGCACCATGGGGGCCTGCT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 ATCINAAGGGGGAAACTCGTTGGGGAGAGGATCTINAGGACAACCCAGNGGGCCATGGNG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 CCACATGGG-----AAAGCTTGTGGGTAGGAATTCTGATACCAACCGGGAGGCCCTGGAA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 ccrecrecregegerearescrercreaaescrercaesaacceccaccreareaccasea 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.6%; Score 156.4; DB 14; Length 494; 59.4%; Pred. No. 1.7e-27; ive 0; Mismatches 184; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Building 30, Room 405, Bethesda, MD 20892
Tel: 3014962111
Fax: 3014020897
                                                                                                                                                                                                                                                                                                               1. .494

'Organism="Rattus norvegicus"

/strain="Sprague-Dowley"

/db_xref="taxon:10116"

/clone="Y358"
                                                                                                                                                                                                                                            Email: yamada@yoda.nidr.nih.gov
Seq primer: AACAAAAGCTGGAGCTCCACC.
Location/Qualifiers
                                        J. Dent. Res. 74, 307-312 (1995)
95181657
                            the rat incisor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277; Conservative
                                                                                           Contact: Yamada Y
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379 TITACIGCAAAGACCAGCACCAIGGGGGCCTGCTCCACAIGGGAAAGCTIGIGGGIAGGA 438
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Fax: 301 443 9890
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AW049121/c
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                                                                    AW920286 594 bp mRNA linear EST 25-MAY-2000 EST351590 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIGT45 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                               I (Dases 1 to 594)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Rat gene index, normalized rat, norvegicus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CCCAGGCCTTCCCCACCACGAAGAGAATCAGGATGTGTCAGGAACGTGGTATTTGAAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 CCAIGGIGGIGGICGAIAAGGACITICCGGAGGACAGGA---GGCCCAGGAAGGIGICCCCCAG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 IGAAAATCAAGACCCIGGAAGGGGCCAACCIGCAAGTGAAGTICACTGICCIGAITICAG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 GACGGTGCCAGGAGAGTGAGCACTGTCCTAGAGAAGAAGAGAAGAATGAACACAG 301
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                                                                                                                                                                                                                                                                                                                                                                     Contact: Lee, NE
The Institute for Genomic Research
9712, Wadical Center Drive, Rockville, MD 20850, USA
781: (301)-838-3529
Fax: (301)-838-0208
Email: nhieetigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 146; DB 10; Length 594; ilarity 57.6%; Pred. No. 5.7e-25; Conservative 0; Mismatches 210; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver, embryo, heart, muscle, spleen"/lab_host="SOLR"

    .594
    /organism="Rattus norvegicus"
/db_xref="taxon:10116"
    /clone="RGIGT45"

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Location/Qualifiers
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                                                                                                                                                                               Norway rat.
Rattus norvegicus
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Matches 310; Conserva
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                                   RESULT 14
AW920286
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                                                                                                                         ACCESSION
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/clone_inb=MIR_MARA_MS1_
//clone_inb=MIR_MRA_MS2_
//dev_stage="27-3 days"
//dev_stage="27-3 days"
//dev_stage="27-3 days"
//dev_bost="19100 (life Technologies)"
//dev_bost="19100 (life Technologies)"
//dep_most_stage="1" det !: Site_2: Eco R1; The
polylinker; Site_1: Not !: Site_2: Eco R1; The
NIE_BMAP_MS2 library is a subtracted library derived from NIE_BMAP_MS2 library is a subtracted library derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalams, contex, amygdala, basal
ganglia, pineal gland, striatum, hipocrampus). The driver
used for subtraction consisted of a pool of 5,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_ILB=NIE_BMAP_MS1 library and a pool of 2,000 clones
obtained cord libraries.
TAG_ILB=NIE_BMAP_MS1 library and a pool of 2,000 clones
of the most purp libraries.
TAG_ILB=NIE_BMAP_MS1 libraries.
TAG_ILB=NIE_BMAP_MS1 library and a pool of 2,000 clones
of the map libraries.
TAG_ILB=NIE_BMAP_MS1 libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: MESTGEMII.nih.gov oligo-dr track that was present in the college contained an oligo-dr track that was present in the oligonoclectide that was used to prime the synthesis of first strand cons and therefore this may represent a bonafide poly A tail. The sequence tag present in the cons between the Nori site and the oligo-dr track served to identify it as a clone from the normalized olfactory bulbs library cDNs inhary Preparation: M.B. Soares tab Clone distribution: NIH BMAP cDNR clones will be made available by the means that is soon to be determined. When NIH record will be updated accordingly when that means is determined accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW049121
UI-M-BHI-amt-h-10-0-UI.81 NIH_BMAP_M_S2 Mus musculus CDNA clone
UI-M-BHI-amt-h-10-0-UI 3', mRNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
439 ATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGGAC 498
                                                                                                                                                            499 ICTCGGAGGAGGACATITICACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACATA 556
                                                                                                                                                                                                                                                                                                                                  Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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/clone="UI-M-BH1-amt-h-10-0-UI"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
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TAG_SEQ=CATGG*
112 a 109 c 123 g 157 t
          BASE COUNT
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Gaps	305	365 378	422	482	542 198	138	
	C-1	AGG AAT	ATGGGA ATGGGA	11. 11. 11. 11.	13GC	AGA -	
Length 501; indels 4;	GGAG	CAGG	CATG	GAAA GAAT	AAGC TAAA	TTC	
igth 21s	CAGP	7365	7007 11000	TTAA	CGGG	CTAC	
Lengt	SAAG SAAA	SGAGC AAAGP	3C 	AGAAT I I I I I	SCAG2	CACC	
)B 10; -18; 152;	recec 	IGCAC I I I IGGAA	SCCTO	rggar rggar	CCTC	SAGC IIIII	
DB 2e-1 5 1	CTGA GTGA	TACC	6666 666A	GCCC!	ACGC GTGC	TCCAC AGCTC	
Score 119.8; DB 10; Pred. No. 1.2e-18; ; Mismatches 152; 1	AAIC AIIC	CAIG 	CCAT	GGAG AGAG	TTTC GTTT	CACC	632
isma	AGAA TTAA	AGCT 	AGCA 	ACCG ATCC	ACAT	TCTG 	21-0 1-0 1-0
Score 119.8; Pred. No. 1.26 0; Mismatches	CAGA 	AGGA	AGGCC	GAAA	GAGG) - - - -	TACC
18;	246 TTCATGAGGGAGGATGGGTGCAGAAGAAAVCCTGATGGGGAAGAGGGGGGGGT 305 	GGCAAATACAGCGCCTATGGGGCCAGGAACTCATGTACCTGCAGGACTGCCCAGGAGG 	GACCACTACATUTTITACTGCAAAGACCAGCACCATGGGGCCTGCTCCACATGGGA 	AAGCTTGTGGGTAGGAATTCTGATACCAACCGGGGAGCCCTGGAAGAATTTAAGAATTG 482 	GTGCAGCGAAGGGACTCTCGGAGGACATTTTCACGCCCCTGCAGACGGAAGCTGC	GFTCCGAACACTAGGCAGC-CCCGGGTCTGCACCTCCAGAGCCCACCTACCTACCAGAGT	602 CACAGAGCCGGACCACCTGGACCTACCCTC 632
17. larity 60. Conservative	CGGT 1 CALT	TATG	TACT	AATT GACT	5-5 5-5	GCAG HHH GCAG	ACCT
ty erva	GGAT TGGT	2000 	CITT IIIC	TAGG 	GGGA GAAT	CTAG	GACC
lari	GGGA	ACAG	ACAT	77666 1111	GCAA	AACA GTGA	9999E
ch 11 Simi 235;	ATG2	AAA 	CACT	CTTG	CAGC	CCCG	agag aagc
fatch scal	TI -		GA = GA	AA — AA	GTG	FE - FE	CAC ACC
Query Match Best Local Similarity Matches 235; Conser	246	306	366	317	483	543 197	602
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Search completed: February 10, 2003, 04:58:27 Job time : 1927.58 secs

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SCHAMAKIES	Result Query No. Score Match Jenath DB ID Description	68 100.0 68 6 AR112296 AR112296 68 100.0 68 6 AR123661 AR123661	68 100.0 68 6 AR128084 AR128084 68 100.0 68 6 AR152175 AR	100.0 68 6 ARL95042 100.0 68 6 AR204656 100 68 6 AR204656	68 100.0 68 6 AR210767 AR210767 Sequence 68 100.0 68 6 AX240681 AX240681 Sequence	10 68 100.0 68 6 BD007433 BD007433 11 64 94.1 68 6 AR112297 AR112297	12 64 94.1 68 6 13 64 94.1 68 6	15 64 94.1 68 6 AR204657 AR204657 AR204657	64 94.1 64 94.1 64 94.1 68 6	54 79.4 559 I AP244627 54 79.4 1359 IO MUSHAPIGB	24 54 79.4 2174 1 25 54 79.4 2544 6 26 54 79.4 2606 6	54 79.4 2606 6 AR089154 54 79.4 3160 12 PSVSPORT	54 79.4 4109 12 PSPORT1 U12390 C		42 61.8 3133 6 AR138969 40 58.8 2288 6 AR064706	40 58.8 2288 6 AR089153 AR089153 38.4 56.5 244 6 AX201441 AX201441	38.4 56.5 37 54.4	41 36.4 53.5 371 1 AF244607 42 31.4 46.2 4566 12 AF177933	4733 435 533	OMNONANATIK	ALLICANTERYS	RESULT 1 AR112296	z	ACCESSION AR112296 VERSION AR112296.1 GI:14092196	WS.	<pre>Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D Roberts-Rapp,L.; Russell,J.C., Stroupe,S.D. and Yu,H.</pre>
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.		M nucleic - nucleic search, using sw model	un on: February 9, 2003, 22:02:40; Search time 221.524 Seconds (without alignments) 8933.518 Million cell updates/sec	US-09-099-823-6	erieul stole: oo equence: 1 AGCICGGAATICCGAGCTIGAGCICGTCGACCCGGGAATI 68	coring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	earched: 2054640 seqs, 14551402878 residues	otal number of hits satisfying chosen parameters: 4109280	inimum DB seq length: 0	ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	atabase : GenEmbl:* 1: gb_ba:*	3: 92_nrg:* 3: 92_in:* 4: 92_0n:*	5: gb_ov:* 6: gb_pat:*	7: 9b_ph:* 8: 9b_pl:* 8: 9b_pl:*	9: 90.0r;* 10: 90_ros* 11: qr sfs:*			10: em_tui: 11: em_tui: 18: em_tii:*		21: em_or:* 22: em_ov:* 23: em_pet:*					34: em_htq_mus:* 34: em_htq_mis:* 35: em_htq_rod:*		 41: em_ntgo_other:*

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PAT 08-AUG-2001
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Cohen, M., Colpitts, T.L., Friedman, P.N., Granados, E.N., Klass, M.R.,
Kussell, J.C. and Stroupe, S.D.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 635083-A 5 26-FEB-2002;
Location/Qualifiers
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In (bases 1 to 68)

Cohen, M., Colpitts, T.L., Friedman, P.N., Granados, E., Klass, M.R.,
Russell, J.C., Stewart, K.D. and Stroupe, S.D.

Serine procease reagents and methods useful for detecting and
treating diseases of the prostate

Patent: US 6222456-4 9 15-WAY-2001;
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                                                                                                    1 AGCICGGAATICCGAGCTIGGATCCICIAGAGCGGCCGCCGACIAGIGAGCICGICGACC 60
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100.03; Score 68; DB 6; Length 68;
Best Local Similarity 100.03; Pred. No. 56-12,
Matches 68; Conservative 0; Mismatches 0, Indels
                                         ; Score 68; DB 6; Length 68;
; Pred. No. 5e-12;
0; Mismatches 0; Indels
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Sequence 9 from patent US 6232456.
AR152175
AR152175.1 GI:15118225
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Sequence 5 from patent US 6350583.
AR195042
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U fbases 1 to 68)

Billing-Wedel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Grandos, E.N., Bodges, S.C., Klass, M.R., Kratochvil, J.D.,
Gordon, J., Russell, J.C. and Stroupe, S.D.
Reagents and methods useful for detecting diseases of the breast
Patent US 6183952-A 5 06-FBB-2001,
Location/Qualifiers

J. . 68

/organism="unknown"
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Patent: US 6130043-A 17 10-OCT-2000;
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disease
Patent: US 6171787-A 11 09-JAN-2001;
Location/Qualifiers
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Sequence 11 from patent US 6171787.
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Sequence 5 from patent US 6183952.
AR128084.1 GI:14115746
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/organism="unknown"
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ARī23661.1 GI:14109022
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[ (bases I to 68) all ing-weel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granded, P.A., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D. Reagents and methods useful for detecting diseases of the prostate Patent: us 6391543-A il 21-MAY-2002; Location/Qualifiers
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/organism-"synthetic construct"
/db_xref="taxon:32650"
/note="Restriction site"
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AR210767
AR210767.1 GI:21513583
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Sequence 7 from Patent W00165262.
AX240681.
AX240681.1 GI:15797664
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13 a 20 c 21 g
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AR210767
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Unclassified.
1 (bases 1 to 68)
Colpitts, T.L.
Reagents and methods useful for detecting diseases of the breast
Patent: US 637671-A 3 30-APR-2002;
Location/Qualifiers
                        Gaps
                                                                                              1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
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1 (bases 1 to 68)

Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,

Hayden, M., Klass, M.R., Roberts-Rapp, L., Russell, J.C. and
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Reagents and methods useful for detecting diseases of the gastrointestinal tract
Patent: 105 636872.A 19 09-APR-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 68; Conservative 0; Mismatches 0; Indels
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Sequence 19 from patent US 6368792.
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AR204656.1 GI:21502038
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Sequence 3 from patent US 6379671.
AR207544 AR207544 1 G1:21507325
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1 (bases 1 to 68)

Balling-Medl,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Grandos,E.N., Hödges,S.C., Klass,M.K., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 18 10-oCT-2000;
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Wiley,S.R.
Member of the TWF family useful for treatment and diagnosis of disease
Patent: US 6171787-A 12 09-JAN-2001;
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Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
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Sequence 12 from patent US 6171787.
AR123662.1 GI:14109023
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Sequence 6 from patent US 6183952.
AR128085 1 GI:14115747
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20 c 19 g
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Medial, Pa. B., Cobhen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R.,
Russell, J.C. and Stroupe, S.D.

Rassell, J.C. and method useful in detecting mammary diseases
Patent: JP 200150380-A 6 27-MAR-2001;
ASBOTT LABORATORIES
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R KLASS,
PULIAN GORDON, EDWAND N GRANADOS, STEVEN C HODGES, PI MICHAEL
RIASS,
PI JOHN D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, PI
STEVEN D STROPPE
PC CLIANIS/09, A61K39/395, A61K39/395, A61P35/00, COTK14/47,
PC COTK16/30,
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1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGTCGACC 60
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                                                                                                                                       Reagent and method useful in detecting mammary diseases. BD007433. BD007433. GI:18635804 UP 2001503980-A/6.
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Sequence 18 from patent US 6130043.
AR112297 1 G1:14092197
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/organism="unidentified"
/db_xref="taxon:32644"
13 a 20 c 21 g 14
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31-OCT-1996 US 08/74206
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JP 2001503980-A/6
27-MAR-2001
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AR112297/c
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5 CGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACCCGGG 64
                                                                                                                                                                                                    68 CGGAATTCCGAGCTTGGATCCTCTAGAGCGCCCCCGACTAGTGAGCTCGTCGACCCCGGG 9
                                                                                                     Query Match 94.18; Score 64; DB 6; Length 68; Best Local Similarity 100.08; Pred. No. 1e-10; Matches 64; Conservative 0; Mismatches 0; Indels
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/organism="unknown"
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Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C. and Stroupe,S.D.
Reagents and method useful for detecting diseases of the breast Patent: WS 6183922A 6 06-PEB-2001;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 68)
Cohen.M., Colpitts,T.L., Friedman,P.N., Granados,E.N., Klass,M.R.,
Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the prostate
Patent: US GSOSBS-A 6 26-FEBS-2002;
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Cohen, M., Colpitts, T.L., Friedman, P.N., Granados, E., Klass, M.R., Russell, J.C., Stewart, K.D. and Stroupe, S.D.
Serine protease reagents and methods useful for detecting and treating diseases of the prostate
Patent: US 6232456-A 10 15-WAY-2001;
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Sequence 10 from patent US 6232456.
AR152176
AR152176.1 GI:15118226
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Sequence 6 from patent US 6350583.
AR195043 AR195043.1 GI:20244480
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Scoring table:

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Human PS190-relate
Human PS190-relate
Synthetic DNA frag
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BS203-related DNA
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PS215 related DNA
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BS203-related DNA
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Human BS274 protei
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Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR;
Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
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                      AAD18675
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AAD13688
AAD13688
AAS07156
AAD57864
AAD35797
AAD34515
AAD34515
AAV63318
AAV63330
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AAX72863
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AAC64930
AAA94072
AAA37697
AAD18676
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AAS07157
AAL40055
AAD35798
AAD35927
AAD34485
                AAA37696
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   (ABBO ) ABBOTT LAB.
  31-MAR-1997;
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Human BS274 protei
                                                    February 9, 2003, 19:57:40; Search time 24.9833 Seconds (without alignments) 6129.540 Million cell updates/sec
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                                                                                                                                                                                                                     1 AGCICGGAATICCGAGCTIG......AGCICGICGACCCGGGAAIT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                   2185239 seqs, 1125999159 residues
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Maximum Match 100%
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                                        OM nucleic - nucleic search, using sw model
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AAX78710
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Database :

WPI; 1998-568280/48.

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This sequence is a fragment of the plasmid pINCY which is used in a method to detect the presence of a target human cS198 polymothcotide in a test sample. The CS198 gene is useful as a marker for gastrointestinal (GI) tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, prognostleating, preventing or treating, or determining the predisposition to diseases and conditions of the GI tract, such as I tract cancer, Barret's oesophagus, gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis, and pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV62335;
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
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                                                                                                                                 The present sequence appears in the specification, which describes a set of contiguous and partially overlapping EST sequences designated CS141. The sequences are isolated from a cDNA library made from gastrointestinal tract tumour and normal tissues. The CS141 gene is useful as a marker for gastrointestinal tract disorders. The methods and products can be used in detecting, diagnosing, staging, monitoring, promosticating, preventing, or determining the predisposition to diseases and conditions of the gastrointestinal tract, such as gastrointestinal tract cancers, Marret's esophagus, gastric ulcer, gastritis leiomyoma, polyps, Crohn's disease, ulcerative colitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST sequence; CS110; gastrointestinal tract; cancer; adenocarcinoma; lymphoma; ss.
New gastrointestinal tract specific polynucleotides, CS141 - used develop products for the diagnosis and treatment of e.g. cancers, gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New CS110 polypeptide(s) - useful for detecting gastrointestinal tract diseases, e.g. gastrointestinal tract cancers and to produce antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence appears in the specification, which describes
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 68; DB 19; Length 68; Best Local Similarity 100.0%; Pred. No. 1.1e-15; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Billing-Medel PA, Cohen M. Colpitts TL, Friedman PN;
Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR;
Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of the specification.
                                                                                               Disclosure; Page 93; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 91; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV63529 standard; cDNA; 68 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CGGGAATT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1998.
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a set of contiguous and partially overlapping EST sequences designated (S110. The sequences are isolated from a colmA library made from gastrointestinal tract tumour and normal tissues. The polypeptides are useful diagnostically to detect CS110 antign/anti-CS110 antibody in samples, e.g. to detect diseases and conditions of the gastrointestinal tract, especially cancers, e.g. adenocarchoma and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGCTCGGBAFTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gastrointestinal tract; Gl tract; cancer; disease; detection; CS198; himan; predisposition; treatment; Barret's oesophagus; gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis; pancreatitis; sa.
                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New gastrointestinal polynucleotides, CS198, and their detection used for developing products for the diagnosis and treatment of gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis
                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 68; DB 19; Length 68; Best Local Similarity 100.0%; Pred. No. 7.1e-15. Maktches 68; Conservative 0; Mismatches 0; Indels
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Gordon J, Granados EN, Hayden M, Hodges EC, Klass MR;
Kratochili JD, Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 98; 127pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pINCY DNA fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US06251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-1999 (first entry)
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CGGGAATT 68

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Human; breast tissue; BS274; detection; disease; marker; antitumour; breast cancer; metastases; atypical hyperplasais; fibroadenoma; cyst; disquosis; therapy; antagonist; cytotoxin; immunoassay; drug screen; chromosomal anomaly; immunisation; antisense; triplex; ribozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Billing-Wedel PA, Cohen M, Colpitts TL, Friedman PN;
Gordon J, Granados BN, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New BS274 nucleic acid as a marker for breast disease
                                                                                               AAV72368 standard; DNA; 68 BP.
                                                                                                                                                                                                           Human BS274 protein primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-347484/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB.
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               W09925850-A1.
                                                                                                                                                                       29-JUL-1999
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                                                                                                                                                                                                                                                                                                                          primer; ss.
                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                   AAV72368;
      61
                                                         RESULT 5
AAV72368
ID AAV72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel contiguous and partially overlapping cDNA sequences and their encoded polypeptides, designated PALS3, transcribed from human pancatic tissue and which have cytostatic activity. The PALS3 polymuclectides, proteins and antibodies are all useful in methods of detection. Detection of PALS3 polymuclectide, antipodies in a sample is indicative of pancratic disease. PALS3 antibodies (antagonists) can also be used in vivo for therapeutic use, e.g. treatment of pancraciic disease, tumnours of metastases. Antisease PALS3 polymuclectides can be used in quentastases. Antisease PALS3 polymuclectides can be used in generation of the pancraciic disease. This sequence represents a pINCX primer than the part of the pancraciic diseases.
                                          Gaps
                                                                      Pancreatic disease; PA153; human; cytostatic; detection; antigen; anti-PA153; antagonist; therapy; treatment; tumour; metastasis; gene therapy; pINCY; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Billing-Wedel PA, Cohen M, Colpitts TL, Friedman PN;
Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
    Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 68; DB 20; Length 68; 1 Similarity 100.0%; Pred. No. 1.1e-15; 68; Conservative 0; Mismatches 0; Indels
100.0%; Score 68; DB 19; Length 66
100.0%; Pred. No. 1.1e-15;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA153 cDNA transcribed from pancreatic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 119; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy of pancreatic diseases. This used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                   03-SEP-1999 (first entry)
Query Match
Best Local Similarity 100.0
Matches 68; Conservative
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                                                                                                                                                  61 CGGGAATT 68
                                                                                                                                                                       61 CGGGAATT 68
                                                                                                                                                                                                                                                                                                                                                                                          pINCY primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09931274-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                 AAX78710;
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97US-0971772. 98WO-DS24562.

(first entry)

RESULT 4

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This invention describes novel human BS274 protein clones which can be used as markers for breast cancer and have antitumour activity. BS274 can also be used as a marker of cancer and its metastases, atypical hyperplasia, fibroadenoma and cysts, so detection/quantification of BS274 encoded polypeptides and BS274-specific antifiodises are used as FA274-specific antifiodises are useful contractions of the diagnosis, staging, monitoring, prognosis, in vivo imaging of, and determining predisposition to these diseases. Antibodises are useful as immunosasy reagents and in competitive drug screens. BS274 nucleic acid and its fragments, are used as probes and primers (in diagnostic assays, for quantifying gene expression, for detecting chromosomal anomalies and the reapoutic antisense, intplex-forming and ribozyme sequences, and for recombinant production of BS274 polypeptides. BS274 polypeptides are used as immunosasay reagents, for generating antibodies, in drug screens used as immunosasay reagents, for generating antibodies, in drug screens cas deal as therapeutic agents) and for rational drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
Disclosure; Page 99; 105pp; English.
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0; Gaps

1 AGCICGGAATICCGAGCTIGGAICCICTAGAGCGGCCGCCGACTAGIGAGCICGICGACC 60

Best Loca Matches

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61 CGGGAATT 68

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The sequence is that of a pINCY polylinker fragment which was used in the construction of an expression vector for a BS124-specific EST clone. Such a clone is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                     New isolated BS124 polynucleotides and polypeptides - used for detecting, diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGCICGGAAIICCGAGCIIGGAICCICIAGAGCGGCCGCCGACIAGIGAGCICGICGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSIO8 gene; prostate disease; benign prostatic hyperplasia; BPH; prostatitis; prostatic intraepithelial neoplasia; PIN; cancer; drug screening; gene therapy; ss.
                                                                                                                                                                                                                           Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;
Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Russell JC, Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 68; DB 20; Length 68; Best Local Similarity 100.0%; Pred. No. 1.1e-15; Matches 68; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 95; 125pp; English.
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                                                                                                                      98WO-US12862.
                                                                                                                                                      97US-0879354.
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                                                                                                                                                                                                                                                                                                      WPI; 1999-105623/09.
                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
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                                                                                                                    19-JUN-1998;
                                                                                                                                                        20-JUN-1997;
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                                                                                   30-DEC-1998.
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AAV71182
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AC AAV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel human breast-specific protein BS200. This protein and its encoding nucleic acids are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                      Breast; cancer; BS200; EST; expressed sequence tag; human; detection; diagnosis; prevention; treatment; disease predisposition; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BS124; breast; cancer; detection; diagnosis; prevention; treatment; pINCY; polylinker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New breast specific gene BS200 - used to develop products for detecting, diagnosing, staging, preventing or treating diseases or conditions of the breast, e.g. breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen M, Colpitts TL, Friedman PN;
s EN, Hodges SC, Klass MR, Kratochvil JD;
pe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 68; DB 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                    Human breast-specific BS200 DNA primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 114; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic pINCY polylinker fragment.
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                                                            AAX37321 standard; DNA; 68 BP.
                                                                                                                                                                                                                                                                                                                                                                                           98WO-US13908.
                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0889127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX07458 standard; cDNA; 68
                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon J, Granados EN,
Russell JC, Stroupe SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-120915/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Billing-Medel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111111
61 CGGGAATT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CGGGAATT 68
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                WO9902714-A1.
                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                    21-JAN-1999
                                                                                                AAX37321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX07458;
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Length 68;

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(see AAA64845 and AAA64846). The present invention relates to a multimeric polypeptide antipen, which comprises of the mammaglobhin and BUJOI proteins. The presence of multimeric polypeptide antigen in a test sample can be used as the basis for a test to diagnose breast disease e.g. breast cancer, in a patient. The detection can be carried out using antibodies specific for the multimeric polypeptide antigen. The present sequence is a synthetic polylinker used in the construction of plasmid pINGY. PINCY was used to clone the coding sequences of mammaglobin and BUJOI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate concer. They can also be used to produce antibodies Which can be used in treatment. The present sequence is one of the PS108 partial coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate cancer; PS108; antibody; tumour; metastasis; vector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methods for detecting target prostate-specific polynucleotides or diseases of the prostate (e.g. prostate anner). comprising detecting the presence of any of 89108 nucleic acid sequences in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                   Cohen M. Colpitts TL, Friedman PN, Gordon J, Granados EN;
Billing-Medel Ps, Klasa MR, Roberts-Rapp L, Stroupe SD, Yu
Kratochvil DP, Russell JC, Hodges SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate-related PS108 vector fragment SEQ ID NO: 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 68; DB 21; Length 68; 100.0%; Pred. No. 1.1e-15;
                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 68; DB 21; Best Local Similarity 100.0%; Pred. No. 1.1e-15; Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                    Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 79-80; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC64929 standard; DNA; 68 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0071710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABBO ) ABBOTT LAB.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CGGGAATT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6130043-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC64929;
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                                                                                                                                                                                                                                                            The present sequence appears in the specification, which describes an enthod for detecting the presence of a target PS108 polymuclectide in a test sample. The method comprises contacting the test sample with at least 1 PS108-specific polymuclacitied or complement, and detecting the presence of the target PS108 polymuclacitie. The products can be used for detecting, diagnosing, staging, anitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatitis, prostatic intraphibalial neoplasia (PTM) and cancer. In particular the products can be used in drug screening and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic polylinker sequence # 1 used in plasmid pINCY construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGCICGGAAITCCGAGCIIGGAICCICIAGAGCGGCCGCCGACIAGIGAGCICGICGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammaglobin and BU101 are members of the uteroglobin protein family.
                                                                                                                 New isolated prostate-specific polynucleotides - used to develop products for the diagnosis and treatment of prostate diseases, e.g. benign hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breast cancer; breast disease detection; mammaglobin; pINCY; uteroglobin; BU101; endometrial; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 68; DB 20; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                  Disclosure; Page 96; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA64847 standard; DNA; 68 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US30489.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colpitts TL, Russell JE;
                                                                     WPI; 1999-034731/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-442366/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABBO ) ABBOTT LAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA64847;
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30-JAN-2001

AAA94071;

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This sequence was used to isolate B3325 coding sequence clones. The invention relates to a method of detecting the presence of a target B3325 propuclectide in a test sample comprises: (a) contacting the test sample comprises: (a) contacting the test sample contacting the test sample and (b) detecting the presence of B3325 polynuclectide or complement thereof; and (b) detecting the presence of B3325 polynuclectide from the test sample. The method is used to enable the identification of certain markers as indicative of a breast tissue disease or condition. The methods can be used for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing, or treating conditions associated with B332, especially breast cancer. The B3325 polypeptides can be used to raise antibodies, and to identify agonists and antipodies. The B3325 polypuclectides are used as a source of probes and primers. The invention provides an alternative, non-surgical diagnostic methods which are capable of detecting early stage breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel methods for the detecting the presence of target B8325 obtypeptides and polymucleotides, used for identifying and monitoring diseases of the breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGCICGGAAIICCGAGCIIGGAICCICIAGAGCGGCCGCCGACIAGIGAGCICGICGACC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 68; DB 21; Length 68; Best Local Similarity 100.0%; Pred. No. 1.1e-15; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      BS325; diagnosis; breast disease; breast cancer; ss.
                                                                                                                                                                                                                                                                                                                                                Linker used to isolate BS325 coding sequence clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 116; 122pp; English.
                                                                                                   AAA37696 standard; DNA; 68 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD18675 standard; DNA; 68 BP.
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                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                    28-OCT-2000
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                                                                                                                                                                                    AAA37696;
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AAD18675
ID AAD186
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AC AAD186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, TGF-beta superfamily; prostate cancer-induced growth factor;
PCIGF; prostate disease; prostate cancer; benign prostatic hyperplasia;
prostatitis; prostatic intraepithelial neoplasia; vector production; ss.
              Gaps
                                                                       1 AGCICGGAAITCCGAGCTIGGATCCTCTAGAGCGGCCGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                           Novel prostate cancer induced growth factor derived polynucleotide useful for detecting, diagnosing, prognosing, preventing or treating conditions of the prostate, especially prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGCICGGAAITCCGAGCIIGGAICCTCTAGAGCGGCCGCCGACTAGTGAGCICGICGACC 60
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    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 114; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA94071 standard; DNA; 68 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Billing-Medel PA, Cohen M,
Russell JC, Stroupe SD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99us-0276600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
Matches 68; Conservative
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WPI; 2000-628218/60.

NAME OF STATES O

(ABBO) ABBOTT LAB.

25-MAR-1999;

WO200056352-A2. Homo sapiens.

28-SEP-2000.

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0; Gaps

61 CGGGAATT 68 CGGGAATT 68

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18-DEC-2001 (first entry)

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The invention relates to a method of detecting the presence of a target CS 198 polynucleotide. The method is useful for least one CS 198 specific polynucleotide. The method is useful for detecting diseases of the gastrointestinal (GI) tract organs.

Getecting diseases of the gastrointestinal (GI) tract organs.

CG particularly cancer. The CS 198 polynucleotides, polypeptides and conditions of the GI tract such as cancer, quastric ulcer, gastritis, Crohn's disease, ulcerative colitis, pancreatitis and parret's esophagus. The CS 198 polypeptides are useful as cancer, gastritis, con's disease, ulcerative colitis, pancreatitis and parret's esophagus. The CS 198 polypeptides are useful as standards or respents in diagnostic immunoassays, as components or as target sites for various therapies. Antibodies directed against at carget sites for various therapies. Antibodies directed against at carget sites for various therapeutic agents, in diagnostic tests and for creening for conditions or diseases associated with CS 198, creening for conditions or diseases associated with CS 198, creening. The method of the invention provides an alternative, non-surgical diagnostic method capable of detecting early stage GI tract disease such as cancer. The present sequence is a synthetic DNA fragment cused for CS 198 for 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 68; DB 22; Length 68; Best Local Similarity 100.0%; Pred, No. 1.1e-15; Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGCCGCCGACTAGTGAGCTCGTCGACC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting the presence of target CS 198 polynucleotide, useful for detecting or diagnosing diseases of the gastrointestinal tract, comprises contacting test sample with at least one CS 198-specific polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Billing-Wedel PA, Cohen M, Colpitts TL, Friedman PN, Gordo
Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 47; 68pp; English.
                                                                               98US-0050516.
                                                                                                                                     97US-0828855.
                                                                                                                                                                                            BILLING-MEDEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                              (KIAS/) KIASS M.R.
(KRAT/) KRATOCHVIL J D.
(ROBE/) ROBERTS-RAPP L.
(RUSS/) RUSSELL J C.
(STRO/) STROUPE S D.
                                                                                                                                                                                                                                           COLPITTS T L.
FRIEDMAN P N.
                                                                                                                                                                                                                                                                                                           GORDON J.
GRANADOS E N.
                                                                                                                                                                                                                                                                                                                                                              HAYDEN M.
HODGES S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-496163/54.
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                                                                                                                                                                                                                        COHEN M
                                                                               30-MAR-1998;
                                                                                                                                  31-MAR-1997;
                         02-AUG-2001.
                                                                                                                                                                                                                                                                                                     (GORD/)
(GRAN/)
(HAYD/)
(HODG/)
(KLAS/)
(KRAT/)
(ROBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A gene or its fragment which codes for a BS106 polypeptide, useful for
the detection of a breast disease such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Billing-Wedel PA, Cohen M, Colpitts II, Friedman PN, Gordon J;
Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human BS106-specific polypeptides and polyunciacorides. The BS106 polypeptides and antibodies are useful for detecting, diagnossing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition of an individual to diseases and conditions of the breast such as breast ancer. They are also useful in the treatment of tumours or metastases. Polymouleachides of the invention are useful in drug screening and gene therapy. The present sequence is a synthetic DNR fragment used to construct pinky plasmid which comprises human BS106 gene oDNA, expressed sequence tag (EST) clone 1662885.
                                                                                            Human; BS106 protein; breast cancer; metastasis; gene therapy; tumour; expressed sequence tag; EST; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 68; DB 22; Length 68; Best Local Similarity 100.0%; Pred. No. 1.1e-15; Matches 68; Conservative 0; Mismatches 0; Indels
                                      Synthetic DNA fragment #1 used to construct plasmid pINCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic DNA fragment #1 for generating pINCY plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 150; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD13638 standard; DNA; 68 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                        29-FEB-2000; 2000US-0516444.
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Gordon J;

WPI; 2001-596773/67.

(ABBO) ABBOTT LAB.

WO200165262-A2.

Synthetic.

07-SEP-2001.

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06-NOV-2001 (first entry)

AAD13638

ID AAD1

XX AAD1

XX AAD1

XX ABD1

XX XX CS N

XX CS 1

KW GS 1

XX CS 3

XX CS 3

XX CS 1

AAD13638;

US2001010904-A1.

Synthetic.

61 CGGGAATT 68

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The patent discloses PS-133 polynucleotides and polypeptides which are indicative of prostate disease. The patent also provides a method for detecting PS133 protein in a test sample. The polynucleotides of the invention are useful for detecting, diagnosing, staging, monitoring, preventing, treating or determining the predisposition of an individual to prostate diseases such as cancer. PS133-derived polynucleotides are used for the detection of normal or altered gene expression, in assays for detecting, amplifying or quantifying genes or nucleic acids relating to prostate tissue diseases and conditions, and to produce probes which can be used in the detection of nucleic acids in a sample. PS-133 proteins are used as immunogens for the therapy. The present sequences are also used in gene therapy. The present sequence is a synthetic DNA fragment which is used in the generation of planty plantid comprising PS133 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                            PS133; prostate disease; cancer; immunogen; gene therapy; cytostatic; pINCY plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New P8133 polynucleotides, useful for detecting, diagnosing, staging, monitoring, prognosing, preventing, treating or determining the predisposition of an individual to a prostate disease, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Granados E, Klass MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 100.0%; Score 68; DB 22; Length 68; Best Local Similarity 100.0%; Pred. No. 1.1e-15; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                         Synthetic DNA fragment #1, to generate pINCY plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 73-74; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen M, Colpitts TL, Friedman PN,
Russell JC, Stewart KD, Stroupe SD;
RESULT 15
AAD14843
ID AAD14843 standard; DNA; 68 BP.
                                                                                                                                                                                                                                                                                                                                       97US-0944483.
                                                                                                                                                                                                                                                                                                                                                                          97US-0944483.
                                                                                                        01-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB.
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                                                                                                                                                                                                                                                                US6232456-B1.
                                                                                                                                                                                                                                                                                                                                     06-0CT-1997;
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                                                                                                                                                                                                                               Synthetic.
                                                                     AAD14843;
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Search completed: February 9, 2003, 22:02:31
Job time : 27.9833 secs

61 CGGGAATT 68

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sequence 26, Appl
sequence 26, Appl
sequence 1, Appl
sequence 5, Appli
sequence 5, Appli
sequence 75, Appli
sequence 17, Appl
sequence 14, Appl
sequence 14, Appl
sequence 10, Appl
sequence 10, Appl
sequence 11, Appl
sequence 11, Appl
sequence 11, Appl
sequence 451, Appl
                                                                                                                                                                                                                                                                                                                                           US-08-689-421-26

US-09-389-528-26

US-09-181-8278-26

US-09-181-8278-26

US-08-181-8278-5

US-08-68-53-849-1

US-09-523-849-1

US-09-523-849-1

US-09-532-849-1

US-09-169-605-14

US-09-169-605-14

US-09-105-5428-11

US-09-105-5428-11

US-09-522-616-451

US-09-522-616-451

US-09-522-616-451

US-09-522-616-451
                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/US/904,/23
RILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
FROM PROPERT:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
FREFERENCE/DOCKET NUMBER: 5997.US.PI
TELECOMMUNICATION INDERR: 5997.US.PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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SEQUENCE CHRACKERSETICS:
LENGTH: 68 Dase pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
552.4
522.4
522.4
442.4
524.4
524.4
53.4
33.4
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37.4
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Sequence 17, Appl
Sequence 11, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 1, Appl
Sequence 11, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 7, Appl
                                                                                                   February 9, 2003, 20:30:25; Search time 4.94273 Seconds (without alignments) 4219.129 Million cell updates/sec
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                                                                                                                                                                                                  1 AGCICGGAAITCCGAGCITG.....AGCICGICGACCCGGGAAIT
                                                                                                                                                                                                                                                                                                                882724
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:: /cpu2_6/ptodata/l/ina/bacvts.seg:*
:: /cpu2_6/ptodata/l/ina/bacxtflles1.seg:*
              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-964-725-6
US-09-071-710-17
US-08-883-086-11
US-08-912-276-5
US-08-912-276-5
US-09-525-397-17
US-09-526-883-11
US-09-215-818-3
US-09-215-818-3
US-09-215-818-3
US-09-215-818-3
US-09-215-818-3
US-09-215-818-3
US-08-944-483-10
US-09-56-883-111-1
US-09-56-883-11-1
US-09-56-883-11-1
                                                                                                                                                                                                                                                                                441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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68
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Match Length
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Perfect score:
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Database :

Result No.

Sequence:

Run on:

Searched:

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1 AGCICGGAATICCGAGCIIGGAICCICIAGAGCGGCCGCCGACIAGIGAGCICGICGACC 60
                                                                                                        Query Match
100.0%; Score 68; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 8.2e-16, No. 8.2e-16, Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MEMBER OF THE THE FAMILY USEFUL TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE CORRESPONDENCES:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6134.US.01
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Patcht No. 083952
GENERAL INFORMATION:
FEMINAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGGENT INFORMATION:
NAME: POTENDEAL, PTISCILLE E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US
TELECOMPRICATION INFORMATION:
TELEPHONE: 847-337-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08883086; Patent No. 6171787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | INFORMATION FOR SEQ ID NO: 115
| SEQUENCE CHARACTERISTICS:
| LENGTH: 68 base pairs | TYPE: nucleic acid | STRANDEDNESS: single | TYPE: TYPE: nucleic acid | TYPE: nucleic acid 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILEY, STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60004-5500
COMPUTER READABLE FORM:
TOTAL TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: WILEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                           61 CGGGAATT 68
                                                                                                                                                                                                                           61 CGGGAATT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-883-086-11
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US-08-912-276-5
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                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                         1 AGCICGGAATICCGAGCTIGGAICCICIAGAGCGGCCGCCGACTAGTGAGCICGICGACC 60
                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INCURANTION INLING-MEDEL, PATRICIA
APPLICANT: COLEN, MAURICE
APPLICANT: COLENTY, TRACET L.
APPLICANT: COLENTY, TRACET L.
APPLICANT: COLENTY, TRACET L.
APPLICANT: GENON, UDLIAN
APPLICANT: GENANDOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: MASSI, MICHAEL R.
APPLICANT: RASSIL, JOHN D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUTE, STERHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
NUMBER OF INVENTION: ROB DETECTING DISEASES OF THE PROSTATE
NUMBER OF SUGURNICES: 41
NUMBER OF SUGURNICES AND METHOR NUMBER OF SUGURNICES
AND METHOR NUMBER OF SUGURNICES AND METHOR NUMBER OF SUGURNICES AND METHOR NUMBER OF SUGURNICES AND METHOR NUMBER OF SUGURNICES AND METHOR NUMBER OF SUGURNICES AND METHOR NUMBER OF SUGURNICES 
                                                                                    ch 100.0%; Score 68; DB 2; Length 68; 1 Similarity 100.0%; Pred. No. 8.2e-16; 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 68; DB 3; Length 68; Best Local Similarity 100.0%; Pred. No. 8.2e-16; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: PASSEEG for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/071,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6083.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 17, Application US/09071710
; Patent No. 6130043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/850,713
PLING DATE: 02-MAY-1597
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKER NUMBER: 608
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 847/938-2623
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CGGGAATT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-071-710-17
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US-09-071-710-17
US-08-964-725-6
                                                                                                                                                                         Matches
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APPLICANT: STROUPE, STRVEN D.
TITLE OF INVENTION: NOVEL SERVEN SERVEN STRUE STRUE STRUE STRUE SERVEN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGCICGGAAITCCGAGCTIGGAICCICIAGAGCGGCCGCCGACIAGIGAGCICGICGACC 60
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Patent No. 6552047

Patent No. 6552047

Patent No. 6552047

Patent No. 6552047

APPLICANT: BILLING-MEDEL, PATRICIA

APPLICANT: COHEN, MAURCE

APPLICANT: GRENAN, PAULA N.

APPLICANT: GRANDOS, EWWARD N.

APPLICANT: GRANDOS, EWWARD N.

APPLICANT: GRANDOS, STEWARD N.

APPLICANT: KRANCCHYLL, JON D.

APPLICANT: KRANCCHYLL, JON D.

APPLICANT: ROBERTS-RAPP, LISA

APPLICANT: STROUPE, STEMPEREN D.

APPLICANT: STROUPE, STEMPEREN D.

TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTRIE

TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Score 68; DB 4; Length 68; Best Local Smilarity 100.0%; Pred, No. 8.2e-16; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATES: USA
COUNTER: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ fOR Windows Version 2.0
CURRENT APILCATION DARA:
APPLICATION NUMBER: US/08/944,483
CLASSIFICATION NUMBER: US/08/944,483
FILING DATE:
FILING DA
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SEQUENCE CHARACTERISTICS:
LENGHH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                   APPLICANT: STEWART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-944-483-9
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US-09-525-397-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Russell, John C.
APPLICANT: Stronpe, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbort Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 68; DB 4; Length 68; Best Local Similarity 100.0%; Pred. No. 8.2e-16; Matches 68; Conservative 0; Mismatches 0; Indels
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COUNTRY: USA
2.P. 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
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APPLICANT: COLETTS, TRACET L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
                                                                                                                                                              Gordon, Julian
Granados, Edward N.
Hodges, Steven C.
Klass, Michael R.
Kratochvil, Jon D.
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ATTORNEY AGREY INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/FOCKEY WUMBER: 5972
TELECOMMUNICATION INFORMATION:
TELEPONE: 847/938-1729
TELEPONE: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
Cohen, Maurice
Colpitts, Tracey L.
Friedman, Paula N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CRARACTERISTICS:
TENTE: nucleic acid
STREE: nuc
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-944-483-9
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APPLICANT: COHEM, MARKE
APPLICANT: COLFITTS, TRACET I.
APPLICANT: RIBEMAM, PAULA N.
APPLICANT: RIBEMAM, MARK
APPLICANT: RIBEMAM, MARK
APPLICANT: ROBERTS-RAPP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS FOR THE
TITLE OF INVENTION: TRACET
WINDERS OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACET
WINDERS OF THE GASTROINTESTINAL
                                                                                                                                                                                                                     1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                    1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGCCGACTAGTGAGCTCGTCGACC 60
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                                                                                                                   Query Match 100.0%; Score 68; DB 4; Length 68; Best Local Similarity 100.0%; Pred. No. 8.2e-16; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.0%; Score 68; DB 4; Length 68; Best Local Similarity 100.0%; Pred. No. 8.2-e.16; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOTER: IBM COMPACTUALE
OPERATING SYSTEM: DOS
SOFTMARE: FASTEST OF Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BILLING-MEDEL, PATRICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6068.US.PI
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PRIOR PEPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/828,856
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35.441
REPERENCE/DOCKET NUMBER: 6068-US.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09049698
Patent No. 6368792
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: IL
COUNTRY: USA
ZIP: GO064-3500
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
TYPE: DNA
CORGANISM: Homo sapiens
US-09-566-876-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-049-698-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGCICGGAATICCGAGCITGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERERAL TREPRANTION:
APPLICANT: Abbott Laboratories
APPLICANT: Ochitts, Tracey L.
APPLICANT: Cochitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Friedman, Paula N.
APPLICANT: Friedman, Paula N.
APPLICANT: Klass, Michael R.
APPLICANT: Russell, John D.
TITLE OF INVENTION: BRAGENES AND METHODS USEFUL FOR TITLE OF INVENTION: DETECTING DISEASES OF THE PROSTANT FILE REFERENCE: 6171.US.PI NOMBER: US/9/566,876
CURRENT FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: US/9/56,509
PRIOR APPLICATION NUMBER: US/9/96,509
PRIOR PRING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
SOFFWARR: FRASER FOR Windows Version 3.0
SEQ ID NO 5
LENGTH: 68
                                                                                                                                                                                                                                                          COMPOTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6083.US.P1
           NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIPICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Becker, Cheryl L.
REGISTRALTON KOMESER: 35,441
REFERENCE/DOCKET NUMBER: 6683.
TELECOMMNISCRITON INFORMATION:
TELECOMMNISCRITON 17935-1729
TELEFRORE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09566876
Patent No. 6350583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISCIS: LENGTH: 68 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                          CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-09-525-397-17
                                                                                                                                                                 COUNTRY: USA
ZIP: 60064-3500
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US-09-566-876-5
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1 AGCICGGAATICCGAGCTIGGAICCICIAGAGCGGCCGCCGACTAGIGAGCICGICGACC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Patent No. 645181

Sequence 2, Application US/09276600

Patent No. 645181

APPLICANT: Patricia Billing-Medel

APPLICANT: Patricia Billing-Medel

APPLICANT: Tracey L. Colpitts

APPLICANT: Tracey L. Colpitts

APPLICANT: Julian Gordon

APPLICANT: Julian Gordon

APPLICANT: John C. Russell

APPLICANT: Stephen D. Stronge

TITLE OF INVENTION: Reagents and Methods Useful for

TITLE OF INVENTION: Detecting Disease of the Prostate

TITLE OF INVENTION: Detecting Disease of the Prostate

CURRENT APPLICATION NUMBER: US/09/276,600

CURRENT FILICATION NUMBER: US/09/276,600

CURRENT FILICATION NUMBER: US/09/276,600

CURRENT FILICATION NUMBER: US/09/276,600

CURRENT FILICATION NUMBER: US/09/276,600
                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION VORBER: US/09/065,383
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/42,385
FILING DATE: 23-APR-1997
ATTORNET/AGENT INFORMATION:
NAME: BECKEY, Cheryl L.,
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.P1
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLECAMINICATION INFORMATION:
TELLECAMINICATION INFORMATION:
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ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 68 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0
Best Local Similarity 100.0
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Single TOPOLOGY: linear US-09-065-383-11
                                                                            COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CGGGAATT 68
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US-09-276-600-2
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             1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                       1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
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                                                                                                                                                                                                                             APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MANCICE
APPLICANT: COLPTITS, TRACET L,
APPLICANT: FRIEDMAN, PRULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-065-383-11

'Sequence II, Application US/09065383

'Patent No. 6391543

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HODGES, STEVEN C. APPLICANT: KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Unknown US-09-215-818-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                    61 CGGGAATT 68
                                                                                               61 CGGGAATT 68
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APPLICANT:
APPLICANT:
APPLICANT:
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5 CGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACCCGGG 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GORDON, JULIAN
APPLICANT: GRANDOS, ENDRARD N.
APPLICANT: GRANDOS, ENDRARD N.
APPLICANT: KLASS, MICHER, R.
APPLICANT: REAFOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: GRROUPE, STEPHEN D.
APPLICANT: GRROUPE, STEPHEN D.
TITLE OF INVENTION: RRAGENTS AND METHODS USBFUL
TITLE OF INVENTION: POR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.1%; Score 64; DB 3; Length 68; Best Local Similarity 100.0%; Pred. No. 2.2e-14; Matches 64; Conservative 0; Mismatches 0; Indels
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OPERATING SYSTEM: DOS
SOFTWARE: FrastSEQ for Windows Version 2.0
CHREMET APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COREN, MANCES
APPLICANT: COLPITS, TRACET I.
APPLICANT: FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY AGENT INPORATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 53,441
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                              RESULT 13
US-09-071-710-18/c
; Sequence 18, Application US/09071710
; Sequence 18, Application US/09071710
; Sequence 18, Application US/09071710
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SEQUENCE CHARACTERISTICS:
LENGHH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
            65 AATT 68
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US-09-071-710-18
                                                                             8 AATT
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                                                                             Gaps
                                                                                                                                          1 AGCICGGAATICCGAGCITGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GORDAN, MAUTICE
APPLICANT: GORDAN, Paula N.
APPLICANT: ENIEDNAN, Paula N.
APPLICANT: ENIEDNAN, Paula N.
APPLICANT: HODGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: RASTOCHTL, Jon D.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: ROSELL, John C.
APPLICANT: ROSELL, John C.
APPLICANT: RASCORPES, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL,
TITLE OF INVENTION: ROW DETECTING DISEASES OF THE LUNG
CORRESPONDENCE ADDRESS:
Query Match 100.0%; Score 68; DB 4; Length 68; Best Local Similarity 100.0%; Pred. No. 8.2e-16; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.1%; Score 64; DB 2; Length 68; Best Local Similarity 100.0%; Pred. No. 2.2e-14; Matches 64; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: OF Windows Version 2.0
SOFTWARE: FastEED for Windows Version 2.0
SURKENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSITGATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5997.US.Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
2.08-964-725-7/C
; Sequence 7, Application US/08964725
; Patent No. 5939265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISCHATION NUMBER: 55,441
REFERENCE/DOCKET NUMBER: 5997
TELECOMOMINACTION INFORMATION:
TELEPRATE 847/938-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CRARACTERISTICS:
LENGHA. 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TIPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-964-725-7
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APPLICANT: WILLEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE TWF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISBASE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
STREET: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 94.1%; Score 64; DB 4; Length 68; Best Local Similarity 100.0%; Pred, No. 2.2e-14; Matches 64; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/0891276
Sequence 6, Application US/08912276
SENERAL INFORMATION:
APPLICANT: Cohen, Maurice
APPLICANT: Cohen, Maurice
APPLICANT: Friedman, Paula N.
APPLICANT: Grandoo, Julian N.
APPLICANT: Gordon, Julian N.
APPLICANT: Granadoo, Edward N.
                                                                                                                                                                                                                                                                                          COUNTEY: USA
ZIF: 6064-3500
COMPUTER READBLE FORM:
MEDJUM TYPE: Diskette
COMFUTER: IBM COMPATIBLE
COMFUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEM VEYSION 2.0
CURRENT APPLICATION NUMBER: US/08/883,086
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: POTEMBARI, PISGILIA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPONE: 847-937-0378
                                            Sequence 12, Application US/08883086
Patent No. 6171787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | INFORMATION FOR SEQ ID NO: 12:
| SEQUENCE CHARACTERISTICS:
| INFORTH: 6B base pairs |
| TYPE: uncleic acid |
| STRANDEDNESS: single |
| TOPOLOGI: linear |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodges, Steven C.
Klass, Michael R.
Kratochvil, Jon D.
Roberts-Rapp, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 847-938-2623
RESULT 14
US-08-883-086-12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AATT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-912-276-6/c
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
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APPLICAMY: Russell, John C.

APPLICAMY: Russell, John C.

TITLE OF INVESTION: REMEMBERS AND METHODS USEFUL
TITLE OF INVESTION: REMEMBERS AND METHODS USEFUL
TITLE OF INVESTION: REMEMBERS AND METHODS USEFUL
TOTAL OF UNIVES:

COMMERC OF SEQUENCE: 25

COMPARE: 100 About Park
STREE: 100 About Park
COMPUTER NEADABLE FORM:

WORTHING STREEM: DAY
COMPUTER THAN COMPATIBLE
COMPUTER MEADABLE FORM:

WORTHING STREEM: DAY
COMPUTER THAN COMPATIBLE
COMPUTER MEADABLE FORM:

WARE: TRANSPORMER: US/08/912.276

COMPUTER THAN COMPATION:

PRIOR APPLICATION NUMBER: 977.US.PI
REMEMBERS APPLICATION NUMBER: 977.US.PI
REMEMBERS APPLICATION NUMBER: 977.US.PI
REMEMBERS: 847/938-1623

TELEMON: 847/938-1623

TELEMON: 847/938-1623

TELEMON: 847/938-1623

TELEMON: 847/938-1623

TELEMON: 847/938-1623

TELEMON: 11 INFORMATION: 6.

SEQUENCE CHARACTERISTICS:
LEMONT: 68 base pairs
TELEMON: 11 INFORMATION: 0.

SEQUENCE CHARACTERISTICS:
LEMONT: 68 base pairs
TOPOLOGY: 1 linear

US-08-912-276-6

OURLY MATCHES 64; CONSETVATIVE 0; MISMATCHES 0; Indels 0; Gaps

OURLY MATCHES 64; CONSETVATIVE 0; MISMATCHES 64; CONSETVATION CONCOURTED CONCOU
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Perfect score:

Run on:

Sequence:

Searched:

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Sequence 4671, Ap Sequence 4207, Ap Sequence 41820, Ap Sequence 9, Appli Sequence 9, Appli Sequence 16, Appli Sequence 17, Appli Sequence 7, Appli Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Appli Sequence 39, Appli Appli Appli Sequence 7, Appli Appli Sequence 39, Appli App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COHEN, MAURICE
APPLICANT: COLDIFIYE, TRACET L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: RICHERL, R.
APPLICANT: RICHERL, OGN C.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE
0. 05-09-878-574-4671

0. 05-09-878-574-4207

0. 05-09-878-574-4207

0. 05-09-878-574-4320

0. 05-09-926-626-9

05-09-092-656-6

05-09-0104-408-26

05-09-0104-408-26

05-09-0104-408-18

05-09-276-600-3

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-09-823-7

05-09-93-7

05-09-93-7

05-09-93-7

05-09-93-7

05-09-93-7

0 05-09-937-7

0 05-09-937-7
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US-09-925-301-39
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SOFWHARE: RestERD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION INVEST: 35,441
REFERENCE, COCKER THRERS: 6158.US.01
TELECOMMUNICATION INFORMATION:
TELEFRONE: 847/938-1729
TELEFRAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08926626
Patent No. US20020035244A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTR: 1L COUNTR: USA 60064-3500
          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
TR-08-926-626-8
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Sequence 7, Appl
Sequence 8, Appl
Sequence 15, Appl
Sequence 10, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 4285, Appl
Sequence 4285, Appl
Sequence 4285, Appl
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Sequence 5, Appli
Sequence 8, Appli
Sequence 25, Appl
Sequence 17, Appl
                                                                                                                                                                                                                                                     (without alignments)
6148.496 Million cell updates/sec
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                                                                                                                                                                                                               February 9, 2003, 21:14:50 ; Search time 5.24229 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                  1 AGCICGGAATICCGAGCTIG.......AGCICGTCGACCCGGGAAIT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO6_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO6_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/PUSOR_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_NEM_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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                                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-926-626-8
US-09-092-296-8
US-09-092-296-8
US-09-104-408-25
US-09-104-408-17
US-09-050-516-28
US-09-050-516-28
US-09-09-09-833-6
US-09-109-833-6
US-09-109-833-6
US-09-109-833-6
US-09-109-838-8
US-09-109-838-8
US-09-109-109-838-8
US-09-878-574-4844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table: IDENTITY_NUC Gapox 1.0
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Maximum DB seq length: 2000000000
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68
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Match Length D
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Database :

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1 AGCICGGAATICCGAGCTIGGATCCTAGAGCGCCGCGACTAGTGAGCTCGTCGACC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09104408
| Publication No. US20020188115al |
| GENERAL INFORMATION: REAGENTS AND METHODS USEFUL |
| TITLE OF INVENTION: REAGENTS AND METHODS USEFUL |
| TITLE OF INVENTION: PRO DETECTING DISEASES OF THE BREAST |
| CORRESSONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDCT Laboratories |
| STREET: 100 Abbort Park Road |
| CORRESSONDENCE ADDCT PARK ROAD |
| CORPER |

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inatch 100.0%; Score 68; DB 9; Length 68; Isocal Similarity 100.0%; Pred. No..4.4e-16; les 68; Conservative 0; Wiematch-1
          APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
TORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: INTEL ACRONDATION COMPUTER: INTEL ACRONDATION CORRECTION CONTRACTOR FOR WINDOWS VERSION 2.0 CURRENT APPLICATION NUMBER: US/09/092,296
FILING DATE: CLASSIFICATION DATA: PRIOR APPLICATION NUMBER: 60/048,810
FILING DATE: 05-JUN-1997
ATTORNEY/ABENT INFORMATION: NAME: Becker, Cheryl L. NAME: Becker, Cheryl L. NEGISTRATION NUMBERS: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IMM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6104.US.01
                                                                                                                                                                                                                                       ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                           STATE: ALL
COUNTRY: USA
ZIF: 60064-3500
COMPUTEN FREADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTEN: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-09-092-296-8
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 8; Length 68
Pred. No. 4.4e-16;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Abbott Laboratories
APPLICANT: Colhen, Maurice
APPLICANT: Colhen, Maurice
APPLICANT: Colhen, Maurice
APPLICANT: Grandso, Tracey L.
APPLICANT: Riassi, Michael R.
APPLICANT: Russell, John C.
APPLICANT: Stronge, Stephen D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
TITLE OF INVENTION: DEFECTING DISEASES OF THE PROSTATE
CURRENT APPLICANTON NUMBER: 2002-02-25
PRIOR APPLICANTON NUMBER: 2002-02-25
PRIOR APPLICANTON NUMBER: 3002-02-25
PRIOR PAPLICANTON NUMBER: 3002-02-25
NUMBER: PRICE OF SEQ ID NOS: 21
SOUTHWERE: FRANCE FILM OF SEQ ID NOS: 21
SOUTHWERE: FRANCE FILM OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 68; DE
Best Local Similarity 100.0%; Pred. No. 4.4
Matches 68; Conservatiye 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BILLING MEDEL, PATRICIA
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Publication No. US20020188114A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICLE
APPLICANT: COLEN, MAURICE
APPLICANT: COLPITS, TRACET I.
APPLICANT: RIEDMAN, PAUJA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10082659
Patent No. US20020168783A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COHEN, MAURICE
COLPITTS, TRACEY I.
FRIEDMAN, PAULA N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
HINFORMATION FOR SEQ ID NO: 8 SEQUENC CHARACTERISTICS: LENGTH: 68 Dase pairs TYPE: nucleic acid STREE nucleic acid STREED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-082-659-5
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-10-082-659-5
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LENGIH: 68
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APPLICANT: COLPITY, TRACEX L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANDOS, EUNARD N.
APPLICANT: GRANDOS, EUNARD N.
APPLICANT: HOSES, STEVEN C.
APPLICANT: HOSES, STEVEN C.
APPLICANT: RIASS, MICHAEL R.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROSERTS-RAPP, LISA
APPLICANT: GROSERTS-RAPP, LISA
APPLICANT: GROSERTS-RAPP, LISA
APPLICANT: FUNENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACET
TITLE OF INVENTION: TAACT
ANDER OF CONTREMENDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 68; DB 9; Length 68; Best Local Similarity 100.0%; Pred. No. 4.4e-16; Matches 68; Conservative 0; Mismatches 0; Indels
    REGISTRATION NUMBER: 35,441
REPRENCE/DOCKET NUMBER: 6188.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEPHONE: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-10-216-408-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Becker, Charyl L. REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
CITY: Abbott Park Road
CITY: Abbott Park Road
STATE: IL
COUNTRY: USA
ZIP: 6064-350
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITIS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/09050516
Patent No. US20010010904A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/428,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                       INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDWSSS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CGGGAATT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: USA
COMPUTER READABLE FORM:
MEDIDW TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIS:
COMPUTER: TASTERS: DOS
SOFTWARE: FASTERS: DOS
SOFTWARE: FASTERS: DOS
SOFTWARE: FASTERS: DOS
SOFTWARE: FASTERS: OS
CURRENT APPLICATION NUMBER: US/10/216,408
FILING DATE: 09-Aug-2002
CLASSIFICATION NUMBER: US/10/216,408
FILING DATE: OF AUG-2002
APPLICATION NUMBER: US/08/959,634
APPLICATION NUMBER: US/08/959,634
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, CHETYL L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: 27
STREET: 110 Abbott Park Road
CITY: Abbott Park
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,408
                                                           CLASSIFTCÁTION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILIKE DATE: 25-JUN-1997
FILIKE DATE: 25-JUN-1997
ATORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl I.
RUGISTRAFION NUMBER:
TELECHAMINICATION INFORMATION:
TELECHAMINICATION INFORMATION:
TELECHAMINICATION INFORMATION:
TELECHAMINICATION INFORMATION:
TELECHAMINICATION INFORMATION:
TELECHAM: 847/938-2623
                                                                                                                                                                                                                                                                                                                 61 CGGGAATT 68
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                                       FILING DATE:
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FRIEDMAN, PAULA N.

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1 AGCICGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
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                                                                                                                                       APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RASOCANLIA, JON D.
APPLICANT: SCHEFFEL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 68; DB 10; Length 68; Best Local Similarity 100.0%; Pred. No. 4.4e-16; Matches 68; Conservative 0; Mismatches 0; Indels Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPUTER: DOS
COMPUTER: RastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6120.US.P1
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Sequence 11, Application US/09234717A
SEMERAL INFORMATION:
APPLICANT: Patriota Billing-Medel
APPLICANT: Marriece Cohen
APPLICANT: Paula N. Friedman
APPLICANT: Paula N. Friedman
APPLICANT: Paula N. Gradon
APPLICANT: Steven C. Gordon
APPLICANT: Steven C. Hodges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099, 823
FILIMG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-UN-1997
ATTORNEY-AGENT HOROMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REPRENCE/POCKER NUMBER: 6120.US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: Abbott Laboratories
100 Abbott Park Road
                                                                                                           HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
RUSSEIL, JOHN C.
                                                                               EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                       GRANADOS, EDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEC ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 68 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 847/938-2623
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Abbott
CITY: Abbott Park
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-09-099-823-6
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                                                                                                               APPLICANT
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Refacit No. US201010101908A1
GENERAL INFORMATION:
APPLICANT: Particla Billing-Wedel
APPLICANT: Maurice Cohen
APPLICANT: Maurice Cohen
APPLICANT: Tracey L. Colpits
APPLICANT: John C. Russell
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for TITLE OF INVENTION: Detecting Disease of the Prostate
FILE REPERMENCE: 6397.US.01 Detecting Disease of CORRENT APPLICATION NUMBER: US/09/276,600
CURRENT APPLICATION NUMBER: US/09/276,600
CURRENT APPLICATION NUMBER: US/09/276,600
NUMBER OF SEQ. ID NOS: 11
SEQ. ID NOS: 11
SEQ. ID NOS: 12
SEQ. ID NOS: 12
SEQ. ID NOS: 13
SEQ. ID NOS: 14
SERVICE SEASER OF MINGOWS VERSION 3.0
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APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Restriction site US-09-276-600-2
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Patent No. US20020018990Al
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                               INFORMATION FOR SEQ ID NO: 28
SEQUENCE CRRACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CGGGAATT 68
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US-09-050-516-28
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US-09-099-823-6
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APPLICANT: Michael R. Klass

TYPE: DNA

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APPLICANT: Patricia Billing-Wedel
APPLICANT: Haurice Cohen
APPLICANT: Tracey L. Colpitts
APPLICANT: Tracey L. Colpitts
APPLICANT: Tracey L. Colpitts
APPLICANT: Julian Gordon
APPLICANT: Garandos
APPLICANT: Steven C. Hodges
APPLICANT: Michael R. Klass
APPLICANT: Michael R. Klass
APPLICANT: John C. Russell
APPLICANT: Steven C. Rossell
APPLICANT: Steven C. Rossell
APPLICANT: Steven C. Russell
A
1 AGCICGGAAITCCGAGCTTGGAICCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
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| Patent No. US20020042049A1
| GENERAL INFORMATION:
| APPLICANT: Russell, John
| APPLICANT: Russell, John
| TITLE OF INVENTION: RRAGENTS AND METHODS USEFUL
| TITLE OF INVENTION: ROW DETECTING DISEASE OF THE BREAST
| NUMBER OF SEQUENCES: 23 DETECTING DISEASE OF THE BREAST
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Abbott Laboratories
| STREET: 100 Abbott Park Road
| STREET: 110 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 68; DB 10; Length 68; Best Local Similarity 100.0%; Pred. No. 4.4e-16; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REPERENCE: 6193.06.F1
CURRENT APPLICATION NUMBER: US/09/193,538A
CURRENT PILIKG DATE: 1998-11-17
EARLIER APPLICATION NUMBER: US 08/971,772
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTENG FOR WINDOWS Version 3.0
EARLIER RASERG for Windows Version 3.0
EARLIER NOS: 23
SOFTWARE: FASTENG FOR WINDOWS VERSION 3.0
EARLIER NOS: 23
EARLIER NOS: 24
EARLIER NOS: 25
EARLIER NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Restriction site US-09-193-538-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09193538A Patent No. US20020037503A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTR: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                            61 CGGGAATT 68
                                                                                                                                                11111111
61 CGGGAATT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CGGGAATT 68
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US-09-193-538-8
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US-09-250-883-15
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                                                                                                                                                                                   셤
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           APPLICANT: John D. Krathochvill
APPLICANT: John D. Krathochvill
APPLICANT: John C. Russell
APPLICANT: Stephen D. Stronge
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of
TITLE OF INVENTION: the Breast
FILE REFERENCE: 6450.108.01
CURRENT APPLICATION NUMBER: US/09/234,717A
CURRENT FILING DATE: 1999-01-21
NUMBER OF SEQ. ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCACTAGTGAGCTCGTCGACCTCGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGACCGCCCCCCACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 68; DB 10; Length 68; Best Local Similarity 100.0%; Pred. No. 4.4e-16; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 68; DB 10; Length 68; Best Local Similarity 100.0%; Pred. No. 4.4e-16; Matches 68; Conservative 0; Mismatches 0; Indels
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APPLICANT: Roberte-Rapp, 1.18a
APPLICANT: SCHOUPE, Stephen D.
APPLICANT: Gordon, Juliano
APPLICANT: Gordon, Juliano
APPLICANT: Gordon, DETECTING DISEASES OF THE BREAST TILLE OF INVENTION: REAGENEYS AND METHODS USEFUL, FOR TILLE OF INVENTION NUMBER: 19/09/850,178
CURRENT FILLING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
PRIOR APPLICATION NUMBER: 1997-11-18
NUMBER OF SEQ. ID NOS: 33
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Billing-Wedel, Fatricia A. Cohen, Waurice Colipitts, Tracey L. Friedman, Faula N. Russell, John C. Granados, Edward N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Restriction site US-09-234-717-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Restriction site
US-09-850-178-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09850178
Patent No. US20020034749A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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Klass, Michael R.
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LENGTH: 68
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APPLICANT: PROTABATION:

APPLICANT: Particia Billing-Medel

APPLICANT: Maurice Cohen

APPLICANT: Tracey L. Colpitts

APPLICANT: Tracey L. Colpitts

APPLICANT: Object and Sordon

APPLICANT: Steven C. Hodges

APPLICANT: Steven C. Hodges

APPLICANT: Steven C. Hodges

APPLICANT: Steven C. Russell

APPLICANT: Steven C. Russell

APPLICANT: Ob D. Kratochvil

APPLICANT: Ob D. Stroupe

TITLE OF INVENTION: Reagenits and Methods Useful for Detecting Diseases of the

TITLE OF INVENTION: Breast

TITLE OF INVENTION: Detecting NUMBER: US/09/215,552

CURRENT FILER PEPERANCE: G192.US. PI

CURRENT FILEND DATE: 1998-12-26

NUMBER OF SEQ ID NOS: 48

SEQ ID NOS: 48

SEQ ID NO 17

LENGTH: 68

LENGTH: 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 68; DB 10; Length 68; Best Local Similarity 100.0%; Pred. No. 4.4e-16; Matches 68; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                   6113.US.01
                                                          11-JUN-1997
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                                                                                                                                                        NAME: BECKET, CRETYL I.
REGISTRATION NUMERS: 35,441
REFERENCE, FOOCKET NUMBER: 6113
TELECOMMUNICATION INFORMATION:
TELEBRONE: 847/938-2623
TELEBRONE: 847/938-2623
INFORMATION FOR SEQ ID NO: 10;
SEQUENCE CHARACTERIFICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Artificial Sequence
        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CGGGAATT 68
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US-09-096-259-10
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US-09-215-652-17
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Ouery Match

Best Local Similarity 100.08; Prod. No. 4.4e-16;

Matches 68; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM Compatible
OCMPOTER: IBM Compatible
SOFRMARE: FastSRO for Windows Version 2.0
SOFRWARE: FastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
CLASSITICATION NUMBER: US/09/250,883
FILING DATE:
APPLICATION NUMBER: US/08/889,316
ATTORNEY AGENT: INFORMATION:
NAME: Becker, Cheryl L.
REGISTRANCHON NUMBER: 35,441
RESPERENCE/COCKET NUMBER: 6131.US.01
TELECOMMUNICATION NUMBER: 6131.US.01
TELECOMMUNICATION NUMBER: 6131.US.01
TELECOMMUNICATION NUMBER: 6131.US.01
TELECOMMUNICATION THYORMATION:
TELECOMMUNICATION THYORMATION:
TELECOMMUNICATION THYORMATION:
TELECOMMUNICATION THYORMATION:
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APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROSERIL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL.
TITLE OF INVENTION: FOR DETECTING DISEASES OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSES: Abbort Laboratories
STREET: 100 Abbott Park Road
STREE: Abbott Park Road
STREE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09096259
Patent No. US20020045164A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY: USA
ZIP: 60064-3500
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61 CGGGAATT 68
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US-09-096-259-10
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| Search completed: February 9, 2003, 22:08:37 | Job time : 6.24229 secs
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APPLICANT: COLETYS, TRACEY L.
APPLICANT: COLETYS, TRACEY L.
APPLICANT: COLETYS, TRACEY L.
APPLICANT: RALBS, MICHAEL N.
APPLICANT: RALBS, MICHAEL R.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REACENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DEFECTING DISEASES OF THE GASTROINTESTINAL.
TITLE OF INVENTION: FOR DEFECTING DISEASES OF THE GASTROINTESTINAL.
TITLE OF INVENTION: PARCT
NUMBER OF SEQUENCES: 25
CORRESPONDENCES: 25
ADDRESSER - ANDRESSER - ANDRESSER.
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Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps
1 AGCTCGGAATTCCGAGCTTGGATCCTCTAGAGCGGCCGCCGACTAGTGAGCTCGTCGACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: Reaf-SEQ for Windows Version 2.0
SOFTWARE: BEAT-CATION DATA:
PRIOR PAPLICATION DATA:
PRIOR PAPLICATION DATA:
FILING DATE: 3.1-MAR-1997
ATTORNEY/AGENT INFORMATION:
REFERRENCE/DOCKET NUMBER: 35,441
REFERRENCE/DOCKET NUMBER: 6066.US.PI
TELECOMMUTATION NUMBER: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                              Sequence 6, Application US/09049695A
Patent No. US20020137904A1
GENBRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; ILBNGTH: 68 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-049-695A-6
                                                                                        61 CGGGAATT 68
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61 CGGGAATT 68
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US-09-049-695A-6
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Scoring table:

Database :

Perfect score:

Run on:

Sequence:

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Sukaryota, Metazoa, Chordata, Urochordata; Ascidiacea, Enterogona; Eukaryota, Metazoa, Chordata, Urochordata; Ascidiacea, Enterogona; Pilebobranchia; Gionidae; Giona.

El 1 (bases 1 to 600)

Sinda, K., Terajima, D., Satake, M., Kawazoe, Y. and Kasuya, A. Sequence taga expressed in hemocytes of Ciona intestinalis

Urpublished (2002)

Urpublished (2002)

Institute of Molecular Immunology

Institute of Development, Aging and Cancer, Tohoku University
Seiryo-machi 4-1, Aoba-ku, Sendai 980-8575, Japan

Tel: 81-22-717-8477

Fax: 81-22-717-847

Fax: 81-22-717-848

Email: satakedidac, tohoku.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ciha301S Ascidian hemocytes cDNA library Ciona intestinalis cDNA, mRNA sequence.
BN960199
BN960199.1 GI:19543626
BI1703139 ff-95f02.x

AG012264 Homo sapi

AG011369 Homo sapi

AG011361 Homo sapi

AG011361 Homo sapi

AG011362 ciha4F205

BM966075 ciha4F205

BM966076 ciha2B15

BM96073 cihaBF218

BM96073 cihaBF218

BM960089 ciha2B15

BM960089 ciha2B15

BM960089 ciha2B15

AG011262 Homo sapi

AG011262 Homo sapi

AG011366 EST388125

AW971301 EST388125

AW9713101 EST388125

AW9713101 EST388125

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AW9713101 EST388129

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AW9713101 EST388128

AW9713101 EST388128

AW9713101 EST388128

AW9713101 EST388138

AW971301 EST388138

AW971301 EST388138

AW971301 EST388138

AW97005 EST388138

AW97068 EST388695

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AW97069 EST388695
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1. .600
/organism="Ciona intestinalis"
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                                                                                                          BM959996
BM960089
AG011876
AG01262
B1807825
B1809564
AL362705
AW973221
AW9731201
AW9731201
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AW974074
AW968194
AW979229
AW972891
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AW972891
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AW969653
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AW973097
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Ciona intestinalis
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BM960199
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     BM960199 cilh301S
AU036326 AU036326
BM960119 cilh3C18S
BM9600836 cilh3120S
BM960064 cilh3130S
AG011933 HOMO Sapi
                                                                                     February 9, 2003, 22:05:30; Search time 189.022 Seconds (without aliquments) 5826.269 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                              1 AGCICGGAAITCCGAGCTIG.....AGCICGICGACCCGGGAAIT
                                                                                                                                                                                                                                             32308132
                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
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9 AU036326
14 BM960119
14 BM960836
14 BM960064
17 AG011933
                                                                 OM nucleic - nucleic search, using sw model
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phiebobranchia; Cionidae; Ciona.

El (bases 1 to 595)

S Shida, K., Terajima, D., Satake, M., Kawazoe, Y. and Kasuya, A. Sequence tages expressed in hemocytes of Ciona intestinalis (Dpublished (2002)

In (Dpublished (2002)

Contact: Masanobu Satake
Contact: Masanobu Satake
Institute of Molecular Immunology
Institute of Development, Aging and Cancer, Tohoku University Serryo-machi 4-1, Aoba-ku, Sendai 980-8575, Japan
Tel: 81-22-717-849

Exx: 81-22-717-849

Exx: 81-22-717-849

Exx: 81-22-717-847

Contaction/Unalifiers

Incedion/Unalifiers

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//docalib-*Residae.tohoku.ac.jp,
//docalib-*Residae.tohoku.ac.jp,
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Enkaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona, Phiebobranchia; Gionidae, Ciona.

Es (Assa, Terajima, D., Satake, M., Kawazoe, Y. and Kasuya, A. Sequence tags expressed in hemocytes of Ciona intestinalis a Gontact: Masanobu Satake

Unpublished (2002)

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Tel: 12-277-8477
Fax: 81-22-77-8477
Fax: 81-22-77-8487
Fax: 81-22-77-847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 79.4%; Score 54; DB 14; Length 595; I Similarity 100.0%; Pred. No. 5.9e-06; 54; Conservative 0; Mismatches 0; Indels
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106 c 105 g 173 t 4 others
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140 c 136 g 128 t 1 c
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Ciona intestinalis
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(Organism="Polyandrocarpa misakiensis" / Artain="White spot" / Artain="White spot" / Artain="White spot" / Ab Artain="White spot" / Ab Artain="Polyandrocarpa misakiensis white spot budding / Clone_lib="Polyandrocarpa misakiensis white spot budding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawamura, K., Hayata, D., Fujiwara, S. and Tubisul, T. Serine protease inhibitors expressed in the process of budding of tunicates as revealed by EST analysis J. Blochem. 124 (5), 1004-1012 (1998)
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Polyandrocarpa misakiensis
Eukaryota Metazoa; Chordata; Urochordata; Ascidiacea;
Solidobranchia; Styelidae; Polyandrocarpa.
1 (bases 1 to 128)
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Pred. No. 4.5e-06;
0; Mismatches 8; Indels 0
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150 a 139 c 139 g 170 t 2 others
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44 c 34 g 25 t
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Kochi University
2-5-1, Akebono-cho, Kochi 780, Japan
Tel: +81-888-44-8313
Fax: +81-888-44-8313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kazuk@cc.kochi-u.ac.jp.
Location/Qualifiers
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AU036326.1 GI:4527287
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                                                                                                                                 Query Match 80.0%;
Best Local Similarity 87.9%;
Matches 58; Conservative
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TITLE
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Danio rerio Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Gypriniformes; Cyprinidae; Danio.

1. Cyprinidae; Danio.

2. Cyprinidae; Danio.

3. Hilliar; L., Rucaba, T., Martin, J., Beck, C., Waiter, W., Eddy, K., Steptoe, M., Theising, B., Allen, M., Bockers, T., Waiter, B., Waller, T., Grabons, M., Pape, D.; Harvey, M., Schurk, R., Ritter, E., Kohn, S., Shillin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R., Materston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIT03139 191 bp mRNA linear EST 18-SEP-2001 fr95f02.xl Zebrafish adult olfactory Danio rerio cDNA clone 5002106 3' similar to SW:CATA_CAMJE Q59296 CATALASE ;, mRNA sequence. B1703139.1 G1:15665768
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CDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Centrol Sequencing by: Washington University Genome
Sequencing Centrol Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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/tiscue_type="adult"
/dev_stage="adult"
/dev_stage="adu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stephen 1. Johnson
Washington University School of Medicine
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                       DD 7. 72 AGCTTGGATCCTCTAGAGCGCCCCCACTAGTGAGCTCGTCGACCCGGGAATT 125
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                                                                                                                                                                                                  Length 756;
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Possible reversed clone: similarity on wrong strand
Seq primer: T7 from Glbco
High quality sequence stop: 181.
Location/Qualifiers
                                                                                                   136 others
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I Similarity 100.0%; Pred. No. 6.1e-06;
54; Conservative 0; Mismatches 0;
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                                                                                                       153 g
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/clone="f61E/X13"
a 142 c 153 g
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Elkaryota, Lo 756)

El (bases 1 to 756)

E Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

L Published Only in DataBase (1998)

E 2 (bases 1 to 756)

E Battori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Direct Submission 1998) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattoriehgc.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fax:0427-88-9561)
                                                                                                                                                                        BM960064 innear EST 18-MAR-2002 oiha2J9S Ascidlan hemocytes cDNa library Ciona intestinalis cDNA,
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Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Masanobu Satake
Department of Molecular Immunology
Institute of Development. Aging and Cancer, Tohoku University
Seliryonachi 4-1. Abba-ku, Sendai 980-8575, Japan
Fax: 81-22-717-8472
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1 (hases 1 to 600)

Shida,K., Terajima,D., Satake,M., Kawazoe,Y. and Kasuya,A.
Sequence tags expressed in hemocytes of Ciona intestinalis
Unpublished (2002)
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//crganism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="hascidian hemocytes cDNA library"
/cell_type="hemocytes"
/dev_stage="hemocytes"
/dev_stage="adult"
/note="Vector: pZil; Site_l: BcoRI"
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       16 AGCTTGGATCCTCTAGAGCGCCCGCCGACTAGTGAGCTCGTCGACCCCGGGAATT 69
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1 Similarity 100.0%; Pred. No. 5.9e-06;
54; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: satake@idac.tohoku.ac.jp.
Location/Qualifiers
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Euthoria; Primates; Catarrhini; Hominidae; Homo.

Entaryota, Ito 644)

Entori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

L. Published Only in DataBase (1998)

E. 2 (bases 1 to 644)

E. 1 (bases 1 to 644)

E. 3 (bases 1 to 644)

E. 3 (bases 1 to 644)

E. 4 (bases 1 to 644)

E. 5 (bases 1 to 644)

E. 5 (bases 1 to 644)

E. 6 (and 1 to 1998) Masahira Hattori, Kitasato University,
Department of Science, 787 Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattorièhgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
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Eukaryotis, Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Bominidae; Homo.

1 (bases 1 to 699)
Eattori, M., 1shi, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q
Eublished Only in DataBase (1998)
Ea (bases 1 to 699)
Ea (bases 2 to 699)
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Homo sapiens genomic DNA, 21q region, clone: B355D16X37, genomic survey sequence.
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/Organism="homo sapiens"
/Organism="homo sapiens"
/Chromosome="21"
/nap="21q"
/Clone="8355D16337"
a 131 c 143 g 154
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/db_xref="taxon:9606"
/chromosome="21"
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/clone="B175P11A94"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes
, Cyprinidae, Danio.
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CDNA. Library Preparation: John Ngai CDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Mashington Distrestity Genome
Sequencing Center Clone distribution: Genome Systems. St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Info@genomesystems.com) and Research Genetics, Buntsville, Alabame
(web address: www.resgen.com) (email contact: info@essen.com)

RessourcenicenicentimarDatenbank, Berlin, Germany (web address:
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/tder_stage="adult"
/der_stage="adult"
/der_stage="adul
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Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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www.rzpd.de)
Possible reversed clone: similarity on wrong strand
Possible reversed clone; similarity on wrong strand
Big prime: T7 from Gibco
High quality sequence stop: 200.
Location/Qualifiers
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/db_xref="taxon:7955"
/clone="5283193"
/clone|lib="Zebrafish adult olfactory"
/sex="mixed"
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BM959632 597 bp mRNA linear EST 18-MAR-2002
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Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 597)
Shida,K., Terajima,D., Satake,M., Kawazoe,Y. and Kasuya,A.
Sequence tags expressed in hemocytes of Ciona intestinalis
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Molecular Immunology
Institute of Development, Aging and Cancer, Tohoku University
Selryo-machi 4-1, Aoba-ku, Sendai 980-8575, Japan
Tel: 81-22-717-8477
Fax: 81-22-717
Fax:
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            Location/Qualifiers
1. 602
/organism="Ciona intestinalis"
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/dev_ztage="adult"
/dev_ztage="adult"
/note=="Vector: pill: Site_l: EcoRI"
/note==Vector: pill: Site_l: BcoRI"
| a 103 c 103 g 169 t 3 others
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110 c 122 g 165 t 2 others
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Battori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo saplens genomic DNA, chromosome 21q

Published Only in DataBase (1998)

Battori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Britished Only in DataBase (1998)

Battori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Direct Submission 1988) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,

Sagamihara 228, Japan (F-mall:hattoriehgc.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Rax:0427-8-9561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enkaryota, Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Pileboranchia; Cionidae; Ciona.

El (basea 1 to 602)

Sida, K., Terajima, D., Satake, M., Kawazoe, Y. and Kasuya, A. Sequence tage expressed in hemocytes of Ciona intestinalis.

Lupublished (2002)

Contact: Masanobu Satake
Department of Molecular Immunology
Institute of Development, Aging and Cancer, Toboku University
Seiryo-machi 4-1, Aoba-ku, Sendai 980-8575, Japan
Tel: 81-22-717-8477
Fax: 81-22-717-847

Email: satake@idac.tohoku.ac.jp.
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602 bp mRNA linear BST 18-MAR-2002 MRAF-2002 mRNA sequence.

EXPLARENCE ACCIDING THE PROPERTY CLOSE THE SET OF T
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                                                      Gaps
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Pred. No. 1.2e-05;
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Pred. No. 1.2e-05;
0; Mismatches 1; Indels
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/organism="Bomo sapiens"
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/db.xrsc="12"
/circonssome="21"
/map="21q"
/clone="B14B21N15"
33 a 162 c 142 g 218
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    Best Local Similarity 98.1%;
Matches 53; Conservative (
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Local Similarity 98.1%;
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 604)

S Shida,K., Terajima,D., Satake,M.; Kawazoe,Y. and Kasuya,A.
S Shida,K., Terajima,D., Satake,M.; Kawazoe,Y. and Kasuya,A.
Sequence tags expressed in hemocytes of Ciona intestinalis
Upublished (2002)

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Enkaryota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.

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Shida.K., Terajina.D., Satake,M., Kawazoe,Y. and Kasuya,A. Sequence tags expressed in hemocytes of Clona intestinalis

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/dlone_lib="Ascidian hemocytes cDNA library"
/del_type="hemocytes"
/dev_stage="adult" site_1: EcoRI"
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//Cll_type="hemocytes"
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